

SEQUENCE LISTING



<110> David Anderson
Constance Berghs
Elina Catterton
Shlomit Edinger
Linda Gorman
Xiaojia (Sasha) Guo
John Herrmann
Ramesh Kekuda
Li Li
Daniel Rieger
Mei Zhong

<120> NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

<130> 21402-593 C

<140> 10/635,398

<141> 2003-08-06

<150> 10/160,619

<151> 2002-06-03

<150> 60/295,661

<151> 2001-06-04

<150> 60/359,122

<151> 2002-02-21

<150> 60/296,404

<151> 2001-06-06

<150> 60/359,035

<151> 2002-02-22

<150> 60/299,949

<151> 2002-06-21

<150> 60/295,607

<151> 2001-06-04

<150> 60/359,964

<151> 2002-02-27

<150> 60/296,418

<151> 2001-06-06

<150> 60/341,562

<151> 2001-12-14

<150> 60/308,890

<151> 2001-07-31

<150> 60/296,575

<151> 2001-06-07

<150> 60/337,477
<151> 2001-12-03

<150> 60/322,297
<151> 2001-09-14

<150> 60/297,414
<151> 2001-06-11

<150> 60/297,573
<151> 2001-06-12

<150> 60/358,978
<151> 2002-02-22

<150> 60/297,567
<151> 2001-06-12

<150> 60/359,121
<151> 2002-02-22

<150> 60/298,285
<151> 2001-06-14

<150> 60/298,528
<151> 2001-06-15

<150> 60/299,133
<151> 2001-06-18

<150> 60/324,669
<151> 2001-09-25

<150> 60/358,656
<151> 2002-02-21

<150> 60/299,230
<151> 2001-06-19

<150> 60/300,177
<151> 2001-06-22

<150> 60/359,034
<151> 2002-02-22

<150> 60/300,883
<151> 2001-06-26

<150> 60/301,530
<151> 2001-06-28

<150> 60/301,550
<151> 2001-06-28

<150> 60/363,676
<151> 2002-03-12

<150> 60/371,346
<151> 2002-04-10

<150> 60/302,951
<151> 2001-07-03

<150> 60/363,430
<151> 2002-03-12

<150> 60/360,858
<151> 2002-03-01

<150> 60/379,444
<151> 2002-05-10

<150> 10/177,809
<151> 2002-06-21

<150> 60/311,285
<151> 2001-08-09

<150> 60/300,290
<151> 2001-06-22

<150> 60/327,892
<151> 2001-10-09

<150> 60/327,345
<151> 2001-10-05

<150> 10/210,130
<151> 2002-08-01

<150> 60/309,501
<151> 2001-08-02

<150> 60/316,508
<151> 2001-08-31

<150> 60/354,655
<151> 2002-02-05

<150> 60/310,291
<151> 2001-08-03

<150> 60/383,887
<151> 2002-05-29

<150> 60/310,951
<151> 2001-08-08

<150> 60/323,936
<151> 2001-09-21

<150> 60/381,039
<151> 2002-05-16

<150> 60/311,292
<151> 2001-08-09

<150> 60/311,979
<151> 2001-08-13

<150> 60/312,203
<151> 2001-08-14

<150> 60/361,764
<151> 2002-03-05

<150> 60/313,201
<151> 2001-08-17

<150> 60/338,078
<151> 2001-12-03

<150> 60/380,971
<151> 2001-05-15

<150> 60/313,156
<151> 2001-08-17

<150> 60/313,702
<151> 2001-08-20

<150> 60/380,980
<151> 2002-05-15

<150> 60/313,643
<151> 2001-08-20

<150> 60/383,761
<151> 2002-05-28

<150> 60/322,716
<151> 2001-09-17

<150> 60/314,031
<151> 2001-08-21

<150> 60/314,466
<151> 2001-08-23

<150> 60/315,403
<151> 2001-08-28

<150> 60/315,853
<151> 2001-08-29

<150> 60/373,825
<151> 2002-04-19

<150> 10/211,689
<151> 2002-08-01

<150> 60/311,751
<151> 2001-08-10

<150> 09/823,172
<151> 2001-03-29

<150> 60/193,664
<151> 2000-03-31

<150> 60/194,614
<151> 2000-04-05

<150> 60/195,063
<151> 2000-04-06

<150> 60/195,066
<151> 2000-04-06

<150> 60/195,067
<151> 2000-04-06

<150> 60/195,068
<151> 2000-04-06

<150> 60/195,069
<151> 2000-04-06

<150> 60/195,070
<151> 2000-04-06

<150> 60/195,510
<151> 2000-04-06

<150> 60/219,855
<151> 2000-07-21

<150> 60/221,284
<151> 2000-07-27

<150> 60/221,325
<151> 2000-07-28

<150> 60/224,588
<151> 2000-08-11

<150> 60/239,613
<151> 2000-10-11

<150> 60/262,508
<151> 2001-01-18

<150> 60/263,604
<151> 2001-01-23

<150> 60/263,433
<151> 2001-01-23

<150> 60/265,161
<151> 2001-01-30

<150> 10/210,712
<151> 2002-08-01

<150> 60/310,544
<151> 2001-08-07

<150> 60/312,892
<151> 2001-08-16

<150> 60/313,415
<151> 2001-08-17

<150> 60/323,994
<151> 2001-09-21

<150> 60/340,233
<151> 2001-12-14

<150> 60/365,478
<151> 2002-03-19

<150> 60/373,814
<151> 2002-04-19

<150> 60/373,989
<151> 2002-04-19

<150> 60/374,632
<151> 2002-04-23

<150> 60/354,591
<151> 2002-02-05

<150> 60/386,971
<151> 2002-06-07

<150> 60/403,732
<151> 2002-08-15

<150> 60/406,392
<151> 2002-08-27

<150> 60/401,597
<151> 2002-08-07

<150> 60/404,829
<151> 2002-08-20

<150> 60/403,574
<151> 2002-08-14

<150> 60/402,248
<151> 2002-08-09

```
<150> 60/403,485
<151> 2002-08-13
```

<160> 146

```
<210> 1
<211> 2239
<212> DNA
<213> Homo sapiens
```

<400> 1																	
tcgccgagcc	cg	tccgccgc	cgcc	atg	gcc	acc	acg	gtg	acc	tgc	acc	cgc				51	
				Met	Ala	Thr	Thr	Val	Thr	Cys	Thr	Arg					
				1	5												
ttc	acc	gac	gag	tac	cag	ctc	tac	gag	gat	att	ggc	aag	ggg	gct	ttc	99	
Phe	Thr	Asp	Glu	Tyr	Gln	Leu	Tyr	Glu	Asp	Ile	Gly	Lys	Gly	Ala	Phe		
10					15	20									25		
tct	gtg	gtc	cga	cgc	tgt	gtc	aag	ctc	tgc	acc	ggc	cat	gag	tat	gca	147	
Ser	Val	Val	Arg	Arg	Cys	Val	Lys	Leu	Cys	Thr	Gly	His	Glu	Tyr	Ala		
				30	35									40			
gcc	aag	atc	atc	aac	acc	aag	aag	ctg	tca	gcc	aga	gat	cac	cag	aag	195	
Ala	Lys	Ile	Ile	Asn	Thr	Lys	Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys		
			45	50									55				
ctg	gag	aga	gag	gct	cgg	atc	tgc	cgc	ctt	ctg	aag	cat	tcc	aac	atc	243	
Leu	Glu	Arg	Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile		
		60	65									70					
gtg	cgt	ctc	cac	gac	agc	atc	tcc	gag	gag	ggc	ttc	cac	tac	ctg	gtc	291	
Val	Arg	Leu	His	Asp	Ser	Ile	Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val		
		75	80									85					
ttc	gat	ctg	gtc	act	ggt	ggg	gag	ctc	ttt	gaa	gac	att	gtg	gcg	aga	339	
Phe	Asp	Leu	Val	Thr	Gly	Gly	Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg		
90					95	100									105		
gag	tac	tac	agc	gag	gct	gat	gcc	agt	cac	tgt	atc	cag	cag	atc	ctg	387	
Glu	Tyr	Tyr	Ser	Glu	Ala	Asp	Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu		
				110	115									120			
gag	gcc	gtt	ctc	cat	tgt	cac	caa	atg	ggg	gtc	gtc	cac	aga	gac	ctc	435	
Glu	Ala	Val	Leu	His	Cys	His	Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu		
			125	130									135				
aag	ccg	gag	aac	ctg	ctt	ctg	gcc	agc	aag	tgc	aaa	ggg	gct	gca	gtg	483	

Lys	Pro	Glu	Asn	Leu	Leu	Leu	Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	
		140					145					150				
aag	ctg	gca	gac	ttc	ggc	cta	gct	atc	gag	gtg	cag	ggg	gac	cag	cag	531
Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	
	155					160					165					
gca	tgg	ttt	ggc	ttc	gct	ggc	aca	cca	ggc	tac	ctg	tcc	cct	gag	gtc	579
Ala	Trp	Phe	Gly	Phe	Ala	Gly	Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	
170					175					180					185	
ctt	cgc	aaa	gag	gcg	tat	ggc	aag	cct	gtg	gac	atc	tgg	gca	tgt	ggg	627
Leu	Arg	Lys	Glu	Ala	Tyr	Gly	Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	
			190					195						200		
gtg	atc	ctg	tac	atc	ctg	ctc	gtg	ggc	tac	cca	ccc	ttc	tgg	gac	gag	675
Val	Ile	Leu	Tyr	Ile	Leu	Leu	Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	
		205					210						215			
gac	cag	cac	aag	ctg	tac	cag	cag	atc	aag	gct	ggc	gcc	tat	gac	ttc	723
Asp	Gln	His	Lys	Leu	Tyr	Gln	Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	
		220				225						230				
ccg	tcc	cct	gag	tgg	gac	acc	gtc	act	cct	gaa	gcc	aaa	aac	ctc	atc	771
Pro	Ser	Pro	Glu	Trp	Asp	Thr	Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	
	235					240					245					
aac	cag	atg	ctg	acc	atc	aac	cct	gcc	aag	cgc	atc	aca	gcc	cat	gag	819
Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	
250					255					260					265	
gcc	ctg	aag	cac	ccg	tgg	gtc	tgc	caa	cgc	tcc	acg	gta	gca	tcc	atg	867
Ala	Leu	Lys	His	Pro	Trp	Val	Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	
				270				275						280		
atg	cac	aga	cag	gag	act	gtg	gag	tgt	ctg	aaa	aag	ttc	aat	gcc	agg	915
Met	His	Arg	Gln	Glu	Thr	Val	Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	
			285				290						295			
aga	aag	ctc	aag	gga	gcc	atc	ctc	acc	acc	atg	ctg	gcc	aca	cgg	aat	963
Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	
		300					305					310				
ttc	tca	gcc	aag	agt	tta	ctc	aac	aag	aaa	gca	gat	gga	gtc	aag	ccc	1011
Phe	Ser	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro	
	315					320					325					
cag	acg	aat	agc	acc	aaa	aac	agt	gca	gcc	gcc	acc	agc	ccc	aaa	ggg	1059
Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly	
330					335					340					345	
acg	ctt	cct	cct	gcc	gcc	ctg	gag	cct	caa	acc	acc	gtc	atc	cat	aac	1107
Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn	
				350				355						360		
cca	gtg	gac	ggg	att	aag	gag	tct	tct	gac	agt	gcc	aat	acc	acc	ata	1155
Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile	

365					370					375					
gag gat gaa gac gct aaa gcc ccc agg gtc ccc gac atc ctg agc tca	1203														
Glu Asp Glu Asp Ala Lys Ala Pro Arg Val Pro Asp Ile Leu Ser Ser															
380 385 390															
gtg agg agg ggc tcg gga gcc cca gaa gcc gag ggg ccc ctg ccc tgc	1251														
Val Arg Arg Gly Ser Gly Ala Pro Glu Ala Glu Gly Pro Leu Pro Cys															
395 400 405															
cca tct ccg gct ccc ttt agc ccc ctg cca gcc cca tcc ccc agg atc	1299														
Pro Ser Pro Ala Pro Phe Ser Pro Leu Pro Ala Pro Ser Pro Arg Ile															
410 415 420 425															
tct gac atc ctg aac tct gtg aga agg ggt tca gga acc cca gaa gcc	1347														
Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala															
430 435 440															
gag ggc ccc ctc tca gcg ggg ccc ccg ccc tgc ctg tct ccg gct ctc	1395														
Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys Leu Ser Pro Ala Leu															
445 450 455															
cta ggc ccc ctg tcc tcc ccg tcc ccc agg atc tct gac atc ctg aac	1443														
Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn															
460 465 470															
tct gtg agg agg ggc tca ggg acc cca gaa gcc gag ggc ccc tcg cca	1491														
Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly Pro Ser Pro															
475 480 485															
gtg ggg ccc ccg ccc tgc cca tct ccg act atc cct ggc ccc ctg ccc	1539														
Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile Pro Gly Pro Leu Pro															
490 495 500 505															
acc cca tgg atg gat gac atc cca ggg ctg ctg cca ccc cca cct gtg	1587														
Thr Pro Trp Met Asp Asp Ile Pro Gly Leu Leu Pro Pro Pro Pro Val															
510 515 520															
ggg aga cac cag act ggg ggt ggt gtg gag ata ctc tta gag aag agg	1635														
Gly Arg His Gln Thr Gly Gly Gly Val Glu Ile Leu Leu Glu Lys Arg															
525 530 535															
ctg ctg ggc cac ggg ctc ggc atg gca ggg cag tgg cta gcc cgg aag	1683														
Leu Leu Gly His Gly Leu Gly Met Ala Gly Gln Trp Leu Ala Arg Lys															
540 545 550															
cag gag atc att aag acc acg gag cag ctc atc gag gcc gtc aac aac	1731														
Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn															
555 560 565															
ggt gac ttt gag gcc tac gcg aaa atc tgt gac cca ggg ctg acc tcg	1779														
Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser															
570 575 580 585															
ttt gag cct gaa gca ctg ggc aac ctg gtt gaa ggg atg gac ttc cac	1827														
Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His															
590 595 600															

aga ttc tac ttc gag aac ctg ctg gcc aag aac agc aag ccg atc cac 1875
 Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His
 605 610 615

acg acc atc ctg aac cca cac gtg cac gtc att gga gag gat gcc gcc 1923
 Thr Thr Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala
 620 625 630

tgc atc gct tac atc cgg ctc acg cag tac att gac ggg cag ggc cgg 1971
 Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg
 635 640 645

ccc cgc acc agc cag tct gag gag acc cgc gtg tgg cac cgc cgc gac 2019
 Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp
 650 655 660 665

ggc aag tgg cag aat gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc 2067
 Gly Lys Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala
 670 675 680

ccg ctg cag tgaagagctg cgccctgggt tcgccggaca gagttggtgt 2116
 Pro Leu Gln

ttggagcccg actgccctcg ggcacacggc ctgcctgtcg catgtttgtg tctgcctcgt 2176

tccctccctt ggtgcctgtg tctgcagaaa aacaagacca gatgtgattt gttaaaaaaa 2236

aaa 2239

<210> 2
 <211> 684
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30
 Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 35 40 45
 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 50 55 60
 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 65 70 75 80
 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 85 90 95
 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
 100 105 110

Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His			
		115					120					125						
Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu			
	130					135					140							
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu			
145					150					155					160			
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly			
				165					170					175				
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly			
			180					185					190					
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu			
		195					200					205						
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln			
	210					215					220							
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr			
225					230					235					240			
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn			
				245					250					255				
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val			
			260					265					270					
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val			
		275					280					285						
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile			
	290					295					300							
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Lys	Ser	Leu	Leu			
305				310					315					320				
Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn			
				325					330					335				
Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu			
			340					345					350					
Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu			
		355					360					365						
Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala			
	370					375					380							
Pro	Arg	Val	Pro	Asp	Ile	Leu	Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala			
385					390					395					400			
Pro	Glu	Ala	Glu	Gly	Pro	Leu	Pro	Cys	Pro	Ser	Pro	Ala	Pro	Phe	Ser			
				405					410					415				

Pro Leu Pro Ala Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val
 420 425 430
 Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly
 435 440 445
 Pro Pro Pro Cys Leu Ser Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro
 450 455 460
 Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly
 465 470 475 480
 Thr Pro Glu Ala Glu Gly Pro Ser Pro Val Gly Pro Pro Pro Cys Pro
 485 490 495
 Ser Pro Thr Ile Pro Gly Pro Leu Pro Thr Pro Trp Met Asp Asp Ile
 500 505 510
 Pro Gly Leu Leu Pro Pro Pro Pro Val Gly Arg His Gln Thr Gly Gly
 515 520 525
 Gly Val Glu Ile Leu Leu Glu Lys Arg Leu Leu Gly His Gly Leu Gly
 530 535 540
 Met Ala Gly Gln Trp Leu Ala Arg Lys Gln Glu Ile Ile Lys Thr Thr
 545 550 555 560
 Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala
 565 570 575
 Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly
 580 585 590
 Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu
 595 600 605
 Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His
 610 615 620
 Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu
 625 630 635 640
 Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu
 645 650 655
 Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His
 660 665 670
 Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
 675 680

<210> 3

<211> 2014

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> (14)..(2011)

 <400> 3
 caccgcatcc acc atg gcc acc acg gtg acc tgc acc cgc ttc acc gac 49
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp
 1 5 10

 gag tac cag ctc tac gag gat att ggc aag ggg gct ttc tct gtg gtc 97
 Glu Tyr Gln Leu Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val
 15 20 25

 cga cgc tgt gtc aag ctc tgc acc ggc cat gag tat gca gcc aag atc 145
 Arg Arg Cys Val Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile
 30 35 40

 atc aac acc aag aag ctg tca gcc aga gat cac cag aag ctg gag aga 193
 Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg
 45 50 55 60

 gag gct cgg atc tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc 241
 Glu Ala Arg Ile Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu
 65 70 75

 cac gac agc atc tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg 289
 His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu
 80 85 90

 gtc act ggt ggg gag ctc ttt gaa gac att gtg gcg aga gag tac tac 337
 Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr
 95 100 105

 agc gag gct gat gcc agt cac tgt atc cag cag atc ctg gag gcc gtt 385
 Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val
 110 115 120

 ctc cat tgt cac caa atg ggg gtc gtc cac aga gac ctc aag ccg gag 433
 Leu His Cys His Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu
 125 130 135 140

 aac ctg ctt ctg gcc agc aag tgc aaa ggg gct gca gtg aag ctg gca 481
 Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala
 145 150 155

 gac ttc ggc cta gct atc gag gtg cag ggg gac cag cag gca tgg ttt 529
 Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe
 160 165 170

 ggt ttc gct ggc aca cca ggc tac ctg tcc cct gag gtc ctt cgc aaa 577
 Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys
 175 180 185

 gag gcg tat ggc aag cct gtg gac atc tgg gca tgt ggg gtg atc ctg 625
 Glu Ala Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu
 190 195 200

tac atc ctg ctc gtg ggc tac cca ccc ttc tgg gac gag gac cag cac	673
Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His	
205 210 215 220	
aag ctg tac cag cag atc aag gct ggt gcc tat gac ttc ccg tcc cct	721
Lys Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro	
225 230 235	
gag tgg gac acc gtc act cct gaa gcc aaa aac ctc atc aac cag atg	769
Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met	
240 245 250	
ctg acc atc aac cct gcc aag cgc atc aca gcc cat gag gcc ctg aag	817
Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys	
255 260 265	
cac ccg tgg gtc tgc caa cgc tcc acg gta gca tcc atg atg cac aga	865
His Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg	
270 275 280	
cag gag act gtg gag tgt ctg aaa aag ttc aat gcc agg aga aag ctc	913
Gln Glu Thr Val Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu	
285 290 295 300	
aag gga gcc atc ctc acc acc atg ctg gcc aca cgg aat ttc tca gtg	961
Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Val	
305 310 315	
ggc aga cag acc acc gct ccg gcc aca atg tcc acc gcg gcc tcc ggc	1009
Gly Arg Gln Thr Thr Ala Pro Ala Thr Met Ser Thr Ala Ala Ser Gly	
320 325 330	
acc acc atg ggg ctg gtg gaa caa gcc aag agt tta ctc aac aag aaa	1057
Thr Thr Met Gly Leu Val Glu Gln Ala Lys Ser Leu Leu Asn Lys Lys	
335 340 345	
gca gat gga gtc aag ccc cag acg aat agc acc aaa aac agt gca gcc	1105
Ala Asp Gly Val Lys Pro Gln Thr Asn Ser Thr Lys Asn Ser Ala Ala	
350 355 360	
gcc acc agc ccc aaa ggg acg ctt cct cct gcc gcc ctg gag cct caa	1153
Ala Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu Glu Pro Gln	
365 370 375 380	
acc acc gtc atc cat aac cca gtg gac ggg att aag gag tct tct gac	1201
Thr Thr Val Ile His Asn Pro Val Asp Gly Ile Lys Glu Ser Ser Asp	
385 390 395	
agt gcc aat acc acc ata gag gat gaa gac gct aaa gcc ccc agg gtc	1249
Ser Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala Pro Arg Val	
400 405 410	
ccc gac atc ctg agc tca gtg agg agg ggc tcg gga gcc cca gaa gcc	1297
Pro Asp Ile Leu Ser Ser Val Arg Arg Gly Ser Gly Ala Pro Glu Ala	
415 420 425	
gag ggg ccc ctg ccc tgc cca tct ccg gct ccc ttt agc ccc ctg cca	1345

Glu Gly Pro Leu Pro Cys Pro Ser Pro Ala Pro Phe Ser Pro Leu Pro	
430	435 440
gcc cca tcc ccc agg atc tct gac atc ctg aac tct gtg aga agg ggt	1393
Ala Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly	
445	450 455 460
tca gga acc cca gaa gcc gag ggc ccc ctc tca gcg ggg ccc ccg ccc	1441
Ser Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro	
	465 470 475
tgc ctg tct ccg gct ctc cta ggc ccc ctg tcc tcc ccg tcc ccc agg	1489
Cys Leu Ser Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg	
	480 485 490
atc tct gac atc ctg aac tct gtg agg agg ggc tca ggg acc cca gaa	1537
Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu	
	495 500 505
gcc gag ggc ccc tcg cca gtg ggg ccc ccg ccc tgc cca tct ccg act	1585
Ala Glu Gly Pro Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr	
	510 515 520
atc cct ggc ccc ctg ccc acc cca tcc cgg aag cag gag atc att aag	1633
Ile Pro Gly Pro Leu Pro Thr Pro Ser Arg Lys Gln Glu Ile Ile Lys	
	525 530 535 540
acc acg gag cag ctc atc gag gcc gtc aac aac ggt gac ttt gag gcc	1681
Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala	
	545 550 555
tac gcg aaa atc tgt gac cca ggg ctg acc tcg ttt gag cct gaa gca	1729
Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala	
	560 565 570
ctg ggc aac ctg gtt gaa ggg atg gac ttc cac aga ttc tac ttc gag	1777
Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu	
	575 580 585
aac ctg ctg gcc aag aac agc aag cca atc cac acg acc atc ctg aac	1825
Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn	
	590 595 600
cca cac gtg cac gtc att gga gag gat gcc gcc tgc atc gct tac atc	1873
Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile	
	605 610 615 620
cgg ctc acg cag tac att gac ggg cag ggc cgg ccc cgc acc agc cag	1921
Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln	
	625 630 635
tct gag gag acc cgc gtg tgg cac cgc cgc gac ggc aag tgg cag aac	1969
Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn	
	640 645 650
gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc ccg ctg cag tga	2014
Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln	

655 660 665
 <210> 4
 <211> 666
 <212> PRT
 <213> Homo sapiens

 <400> 4
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30
 Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 35 40 45
 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 50 55 60
 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 65 70 75 80
 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 85 90 95
 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
 100 105 110
 Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His
 115 120 125
 Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
 130 135 140
 Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
 145 150 155 160
 Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
 165 170 175
 Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly
 180 185 190
 Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu
 195 200 205
 Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln
 210 215 220
 Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
 225 230 235 240
 Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn
 245 250 255
 Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val

260								265				270						
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val			
		275						280					285					
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile			
	290					295					300							
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg	Gln	Thr			
305					310					315					320			
Thr	Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr	Met	Gly			
				325					330					335				
Leu	Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val			
			340					345					350					
Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro			
	355						360					365						
Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile			
	370					375					380							
His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr			
385					390					395					400			
Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Pro	Arg	Val	Pro	Asp	Ile	Leu			
			405					410						415				
Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala	Pro	Glu	Ala	Glu	Gly	Pro	Leu			
		420					425						430					
Pro	Cys	Pro	Ser	Pro	Ala	Pro	Phe	Ser	Pro	Leu	Pro	Ala	Pro	Ser	Pro			
	435					440						445						
Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly	Thr	Pro			
	450				455						460							
Glu	Ala	Glu	Gly	Pro	Leu	Ser	Ala	Gly	Pro	Pro	Pro	Cys	Leu	Ser	Pro			
465					470				475					480				
Ala	Leu	Leu	Gly	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Arg	Ile	Ser	Asp	Ile			
			485					490						495				
Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala	Glu	Gly	Pro			
		500						505					510					
Ser	Pro	Val	Gly	Pro	Pro	Pro	Cys	Pro	Ser	Pro	Thr	Ile	Pro	Gly	Pro			
	515						520					525						
Leu	Pro	Thr	Pro	Ser	Arg	Lys	Gln	Glu	Ile	Ile	Lys	Thr	Thr	Glu	Gln			
	530					535					540							
Leu	Ile	Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	Ala	Tyr	Ala	Lys	Ile			
545					550				555						560			
Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly	Asn	Leu			

	565		570		575
Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu Ala	580		585		590
Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His	595		600		605
Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln	610		615		620
Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu Thr	625		630		635
Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe His	645		650		655
Cys Ser Gly Ala Pro Val Ala Pro Leu Gln	660		665		

<210> 5
 <211> 1998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (1998)

<400> 5	
atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc	48
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu	
1 5 10 15	
tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc	96
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val	
20 25 30	
aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc aag	144
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys	
35 40 45	
aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg atc	192
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile	
50 55 60	
tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc atc	240
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile	
65 70 75 80	
tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt ggg	288
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly	
85 90 95	
gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct gat	336
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp	
100 105 110	

gcc agt cac tgt atc cag cag atc ctg gag gcc gtt ctc cat tgt cac	384
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His	
115 120 125	
caa atg ggg gtc gtc cac aga gac ctc aag ccg gag aac ctg ctt ctg	432
Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu	
130 135 140	
gcc agc aag tgc aaa ggg gct gca gtg aag ctg gca gac ttc ggc cta	480
Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu	
145 150 155 160	
gct atc gag gtg cag ggg gac cag cag gca tgg ttt ggt ttc gct ggc	528
Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly	
165 170 175	
aca cca ggc tac ctg tcc cct gag gtc ctt cgc aaa gag gcg tat ggc	576
Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly	
180 185 190	
aag cct gtg gac atc tgg gca tgt ggg gtg atc ctg tac atc ctg ctc	624
Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu	
195 200 205	
gtg ggc tac cca ccc ttc tgg gac gag gac cag cac aag ctg tac cag	672
Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln	
210 215 220	
cag atc aag gct ggt gcc tat gac ttc ccg tcc cct gag tgg gac acc	720
Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr	
225 230 235 240	
gtc act cct gaa gcc aaa aac ctc atc aac cag atg ctg acc atc aac	768
Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn	
245 250 255	
cct gcc aag cgc atc aca gcc cat gag gcc ctg aag cac ccg tgg gtc	816
Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val	
260 265 270	
tgc caa cgc tcc acg gta gca tcc atg atg cac aga cag gag act gtg	864
Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val	
275 280 285	
gag tgt ctg aaa aag ttc aat gcc agg aga aag ctc aag gga gcc atc	912
Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile	
290 295 300	
ctc acc acc atg ctg gcc aca cgg aat ttc tca gtg ggc aga cag acc	960
Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Val Gly Arg Gln Thr	
305 310 315 320	
acc gct ccg gcc aca atg tcc acc gcg gcc tcc ggc acc acc atg ggg	1008
Thr Ala Pro Ala Thr Met Ser Thr Ala Ala Ser Gly Thr Thr Met Gly	
325 330 335	

ctg gtg gaa caa gcc aag agt tta ctc aac aag aaa gca gat gga gtc	1056
Leu Val Glu Gln Ala Lys Ser Leu Leu Asn Lys Lys Ala Asp Gly Val	
340 345 350	
aag ccc cag acg aat agc acc aaa aac agt gca gcc gcc acc agc ccc	1104
Lys Pro Gln Thr Asn Ser Thr Lys Asn Ser Ala Ala Ala Thr Ser Pro	
355 360 365	
aaa ggg acg ctt cct cct gcc gcc ctg gag cct caa acc acc gtc atc	1152
Lys Gly Thr Leu Pro Pro Ala Ala Leu Glu Pro Gln Thr Thr Val Ile	
370 375 380	
cat aac cca gtg gac ggg att aag gag tct tct gac agt gcc aat acc	1200
His Asn Pro Val Asp Gly Ile Lys Glu Ser Ser Asp Ser Ala Asn Thr	
385 390 395 400	
acc ata gag gat gaa gac gct aaa gcc ccc agg gtc ccc gac atc ctg	1248
Thr Ile Glu Asp Glu Asp Ala Lys Ala Pro Arg Val Pro Asp Ile Leu	
405 410 415	
agc tca gtg agg agg ggc tcg gga gcc cca gaa gcc gag ggg ccc ctg	1296
Ser Ser Val Arg Arg Gly Ser Gly Ala Pro Glu Ala Glu Gly Pro Leu	
420 425 430	
ccc tgc cca tct ccg gct ccc ttt agc ccc ctg cca gcc cca tcc ccc	1344
Pro Cys Pro Ser Pro Ala Pro Phe Ser Pro Leu Pro Ala Pro Ser Pro	
435 440 445	
agg atc tct gac atc ctg aac tct gtg aga agg ggt tca gga acc cca	1392
Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro	
450 455 460	
gaa gcc gag ggc ccc ctc tca gcg ggg ccc ccg ccc tgc ctg tct ccg	1440
Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys Leu Ser Pro	
465 470 475 480	
gct ctc cta ggc ccc ctg tcc tcc ccg tcc ccc agg atc tct gac atc	1488
Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile Ser Asp Ile	
485 490 495	
ctg aac tct gtg agg agg ggc tca ggg acc cca gaa gcc gag ggc ccc	1536
Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly Pro	
500 505 510	
tcg cca gtg ggg ccc ccg ccc tgc cca tct ccg act atc cct ggc ccc	1584
Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile Pro Gly Pro	
515 520 525	
ctg ccc acc cca tcc cgg aag cag gag atc att aag acc acg gag cag	1632
Leu Pro Thr Pro Ser Arg Lys Gln Glu Ile Ile Lys Thr Thr Glu Gln	
530 535 540	
ctc atc gag gcc gtc aac aac ggt gac ttt gag gcc tac gcg aaa atc	1680
Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile	
545 550 555 560	
tgt gac cca ggg ctg acc tcg ttt gag cct gaa gca ctg ggc aac ctg	1728

Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly	Asn	Leu		
				565					570					575			
gtt	gaa	ggg	atg	gac	ttc	cac	aga	ttc	tac	ttc	gag	aac	ctg	ctg	gcc	1776	
Val	Glu	Gly	Met	Asp	Phe	His	Arg	Phe	Tyr	Phe	Glu	Asn	Leu	Leu	Ala		
			580					585					590				
aag	aac	agc	aag	cca	atc	cac	acg	acc	atc	ctg	aac	cca	cac	gtg	cac	1824	
Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	Pro	His	Val	His		
			595				600					605					
gtc	att	gga	gag	gat	gcc	gcc	tgc	atc	gct	tac	atc	cgg	ctc	acg	cag	1872	
Val	Ile	Gly	Glu	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	Ile	Arg	Leu	Thr	Gln		
	610					615					620						
tac	att	gac	ggg	cag	ggc	cgg	ccc	cgc	acc	agc	cag	tct	gag	gag	acc	1920	
Tyr	Ile	Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	Ser	Glu	Glu	Thr		
	625				630				635						640		
cgc	gtg	tgg	cac	cgc	cgc	gac	ggc	aag	tgg	cag	aac	gtg	cac	ttc	cac	1968	
Arg	Val	Trp	His	Arg	Arg	Asp	Gly	Lys	Trp	Gln	Asn	Val	His	Phe	His		
			645					650						655			
tgc	tcg	ggc	gcg	cct	gtg	gcc	ccg	ctg	cag							1998	
Cys	Ser	Gly	Ala	Pro	Val	Ala	Pro	Leu	Gln								
			660					665									

<210> 6
 <211> 666
 <212> PRT
 <213> Homo sapiens

<400> 6																	
Met	Ala	Thr	Thr	Val	Thr	Cys	Thr	Arg	Phe	Thr	Asp	Glu	Tyr	Gln	Leu		
1				5				10						15			
Tyr	Glu	Asp	Ile	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	Arg	Arg	Cys	Val		
			20				25						30				
Lys	Leu	Cys	Thr	Gly	His	Glu	Tyr	Ala	Ala	Lys	Ile	Ile	Asn	Thr	Lys		
		35					40					45					
Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile		
	50					55					60						
Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile		
	65				70					75					80		
Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly		
			85						90					95			
Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp		
		100						105					110				
Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His		
		115					120					125					

Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu			
130						135					140							
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu			
145					150					155					160			
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly			
				165					170					175				
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly			
			180					185					190					
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu			
		195					200					205						
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln			
	210					215					220							
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr			
225					230					235					240			
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn			
				245				250						255				
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val			
			260					265					270					
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val			
		275					280					285						
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile			
	290					295					300							
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg	Gln	Thr			
305					310					315					320			
Thr	Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr	Met	Gly			
				325					330					335				
Leu	Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val			
			340					345					350					
Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro			
		355					360					365						
Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile			
	370					375					380							
His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr			
385					390					395					400			
Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Pro	Arg	Val	Pro	Asp	Ile	Leu			
				405					410					415				
Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala	Pro	Glu	Ala	Glu	Gly	Pro	Leu			
			420					425					430					

Pro Cys Pro Ser Pro Ala Pro Phe Ser Pro Leu Pro Ala Pro Ser Pro
 435 440 445
 Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro
 450 455 460
 Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys Leu Ser Pro
 465 470 475 480
 Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile Ser Asp Ile
 485 490 495
 Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly Pro
 500 505 510
 Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile Pro Gly Pro
 515 520 525
 Leu Pro Thr Pro Ser Arg Lys Gln Glu Ile Ile Lys Thr Thr Glu Gln
 530 535 540
 Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile
 545 550 555 560
 Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu
 565 570 575
 Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu Ala
 580 585 590
 Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His
 595 600 605
 Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln
 610 615 620
 Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu Thr
 625 630 635 640
 Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe His
 645 650 655
 Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
 660 665

<210> 7
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (1809)

<400> 7
 atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu

48

1	5	10	15	
tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc				96
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val	20	25	30	
aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc aag				144
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys	35	40	45	
aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg atc				192
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile	50	55	60	
tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc atc				240
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile	65	70	75	80
tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt ggg				288
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly	85	90	95	
gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct gat				336
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp	100	105	110	
gcc agt cac tgt atc cag cag atc ctg gag gcc gtt ctc cat tgt cac				384
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His	115	120	125	
caa atg ggg gtc gtc cac aga gac ctc aag ccg gag aac ctg ctt ctg				432
Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu	130	135	140	
gcc agc aag tgc aaa ggg gct gca gtg aag ctg gca gac ttc ggc cta				480
Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu	145	150	155	160
gct atc gag gtg cag ggg gac cag cag gca tgg ttt ggt ttc gct ggc				528
Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly	165	170	175	
aca cca ggc tac ctg tcc cct gag gtc ctt cgc aaa gag gcg tat ggc				576
Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly	180	185	190	
aag cct gtg gac atc tgg gca tgt ggg gtg atc ctg tac atc ctg ctc				624
Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu	195	200	205	
gtg ggc tac cca ccc ttc tgg gac gag gac cag cac aag ctg tac cag				672
Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln	210	215	220	
cag atc aag gct ggt gcc tat gac ttc ccg tcc cct gag tgg gac acc				720
Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr	225	230	235	240

gtc act cct gaa gcc aaa aac ctc atc aac cag atg ctg acc atc aac	768
Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn	
245 250 255	
cct gcc aag cgc atc aca gcc cat gag gcc ctg aag cac ccg tgg gtc	816
Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val	
260 265 270	
tgc caa cgc tcc acg gta gca tcc atg atg cac aga cag gag act gtg	864
Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val	
275 280 285	
gag tgt ctg aaa aag ttc aat gcc agg aga aag ctc aag gga gcc atc	912
Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile	
290 295 300	
ctc acc acc atg ctg gcc aca cgg aat ttc tca gcc aag agt tta ctc	960
Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala Lys Ser Leu Leu	
305 310 315 320	
aac aag aaa gca gat gga gtc aag ccc cag acg aat agc acc aaa aac	1008
Asn Lys Lys Ala Asp Gly Val Lys Pro Gln Thr Asn Ser Thr Lys Asn	
325 330 335	
agt gca gcc gcc acc agc ccc aaa ggg acg ctt cct cct gcc gcc ctg	1056
Ser Ala Ala Ala Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu	
340 345 350	
gag cct caa acc acc gtc atc cat aac cca gtg gac ggg att aag gag	1104
Glu Pro Gln Thr Thr Val Ile His Asn Pro Val Asp Gly Ile Lys Glu	
355 360 365	
tct tct gac agt gcc aat acc acc ata gag gat gaa gac gct aaa gcc	1152
Ser Ser Asp Ser Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala	
370 375 380	
ccc agg atc tct gac atc ctg aac tct gtg aga agg ggt tca gga acc	1200
Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr	
385 390 395 400	
cca gaa gcc gag ggc ccc ctc tca gcg ggg ccc ccg ccc tgc ctg tct	1248
Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys Leu Ser	
405 410 415	
ccg gct ctc cta ggc ccc ctg tcc tcc ccg tcc ccc agg atc tct gac	1296
Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile Ser Asp	
420 425 430	
atc ctg aac tct gtg agg agg ggc tca ggg acc cca gaa gcc gag ggc	1344
Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly	
435 440 445	
ccc tcg cca gtg ggg ccc ccg ccc tgc cca tct ccg act atc cct ggc	1392
Pro Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile Pro Gly	
450 455 460	

ccc ctg ccc acc cca tcc cgg aag cag gag atc att aag acc acg gag 1440
Pro Leu Pro Thr Pro Ser Arg Lys Gln Glu Ile Ile Lys Thr Thr Glu
465 470 475 480

cag ctc atc gag gcc gtc aac aac ggt gac ttt gag gcc tac gcg aaa 1488
Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys
485 490 495

atc tgt gac cca ggg ctg acc tcg ttt gag cct gaa gca ctg ggc aac 1536
Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn
500 505 510

ctg gtt gaa ggg atg gac ttc cac aga ttc tac ttc gag aac ctg ctg 1584
Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu
515 520 525

gcc aag aac agc aag ccg atc cac acg acc atc ctg aac cca cac gtg 1632
Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val
530 535 540

cac gtc att gga gag gat gcc gcc tgc atc gct tac atc cgg ctc acg 1680
His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr
545 550 555 560

cag tac att gac ggg cag ggc cgg ccc cgc acc agc cag tct gag gag 1728
Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu
565 570 575

acc cgc gtg tgg cac cgc cgc gac ggc aag tgg cag aac gtg cac ttc 1776
Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe
580 585 590

cac tgc tcg ggc gcg cct gtg gcc ccg ctg cag 1809
His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
595 600

<210> 8
<211> 603
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
1 5 10 15
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
20 25 30
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
35 40 45
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
50 55 60
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
65 70 75 80

Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly		85	90	95
Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp		100	105	110
Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His		115	120	125
Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu		130	135	140
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu		145	150	155
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly		165	170	175
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly		180	185	190
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu		195	200	205
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln		210	215	220
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr		225	230	235
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn		245	250	255
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val		260	265	270
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val		275	280	285
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile		290	295	300
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Lys	Ser	Leu	Leu		305	310	315
Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn		325	330	335
Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu		340	345	350
Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu		355	360	365
Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala		370	375	380

Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr
 385 390 395 400
 Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys Leu Ser
 405 410 415
 Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile Ser Asp
 420 425 430
 Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly
 435 440 445
 Pro Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile Pro Gly
 450 455 460
 Pro Leu Pro Thr Pro Ser Arg Lys Gln Glu Ile Ile Lys Thr Thr Glu
 465 470 475 480
 Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys
 485 490 495
 Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn
 500 505 510
 Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu
 515 520 525
 Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val
 530 535 540
 His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr
 545 550 555 560
 Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu
 565 570 575
 Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe
 580 585 590
 His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
 595 600

<210> 9

<211> 1923

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1923)

<400> 9

atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc	48
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu	
1 5 10 15	

tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc	96
---	----

Tyr	Glu	Asp	Ile	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	Arg	Arg	Cys	Val		
			20					25						30			
aag	ctc	tgc	acc	ggc	cat	gag	tat	gca	gcc	aag	atc	atc	aac	acc	aag	144	
Lys	Leu	Cys	Thr	Gly	His	Glu	Tyr	Ala	Ala	Lys	Ile	Ile	Asn	Thr	Lys		
		35					40					45					
aag	ctg	tca	gcc	aga	gat	cac	cag	aag	ctg	gag	aga	gag	gct	cgg	atc	192	
Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile		
		50					55					60					
tgc	cgc	ctt	ctg	aag	cat	tcc	aac	atc	gtg	cgt	ctc	cac	gac	agc	atc	240	
Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile		
		65				70				75					80		
tcc	gag	gag	ggc	ttc	cac	tac	ctg	gtc	ttc	gat	ctg	gtc	act	ggg	ggg	288	
Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly		
				85					90					95			
gag	ctt	ttt	gaa	gac	att	gtg	gcg	aga	gag	tac	tac	agc	gag	gct	gat	336	
Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp		
			100					105					110				
gcc	agt	cac	tgt	atc	cag	cag	atc	ctg	gag	gcc	gtt	ctc	cat	tgt	cac	384	
Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His		
		115					120					125					
caa	atg	ggg	gtc	gtc	cac	aga	gac	ctc	aag	ccg	gag	aac	ctg	ctt	ctg	432	
Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu		
		130					135					140					
gcc	agc	aag	tgc	aaa	ggg	gct	gca	gtg	aag	ctg	gca	gac	ttc	ggc	cta	480	
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu		
		145				150				155					160		
gct	atc	gag	gtg	cag	ggg	gac	cag	cag	gca	tgg	ttt	ggg	ttc	gct	ggc	528	
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly		
				165					170					175			
aca	cca	ggc	tac	ctg	tcc	cct	gag	gtc	ctt	cgc	aaa	gag	gcg	tac	ggc	576	
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly		
			180					185					190				
aag	ccc	gtg	gac	atc	tgg	gca	tgt	ggg	gtg	atc	ctg	tac	atc	ctg	ctc	624	
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu		
		195					200					205					
gtg	ggc	tac	cca	ccc	ttc	tgg	gac	gag	gac	cag	cac	aag	ctg	tac	cag	672	
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln		
		210				215					220						
cag	atc	aag	gct	ggg	gcc	tat	gac	ttc	ccg	tcc	cct	gag	tgg	gac	acc	720	
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr		
		225				230				235					240		
gtc	act	cct	gaa	gcc	aaa	aac	ctc	atc	aac	cag	atg	ctg	acc	atc	aac	768	
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn		

245										250					255					
cct	gcc	aag	cgc	atc	aca	gcc	cat	gag	gcc	ctg	aag	cac	ccg	tg	gtc	816				
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val					
			260					265					270							
tgc	caa	cg	tcc	acg	gta	gca	tcc	atg	atg	cac	aga	cag	gag	act	gtg	864				
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val					
			275				280					285								
gag	tgt	ctg	aaa	aag	ttc	aat	gcc	agg	aga	aag	ctc	aag	gga	gcc	atc	912				
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile					
	290					295					300									
ctc	acc	acc	atg	ctg	gcc	aca	cg	aat	ttc	tca	gcc	aag	agt	tta	ctc	960				
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Lys	Ser	Leu	Leu					
305					310					315					320					
aac	aag	aaa	gca	gat	gga	gtc	aag	ccc	cag	acg	aat	agc	acc	aaa	aac	1008				
Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn					
			325					330					335							
agt	gca	gcc	gcc	acc	agc	ccc	aaa	ggg	acg	ctt	cct	cct	gcc	gcc	ctg	1056				
Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu					
			340					345					350							
gag	cct	caa	acc	acc	gtc	atc	cat	aac	cca	gtg	gac	ggg	att	aag	gag	1104				
Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu					
		355					360					365								
tct	tct	gac	agt	gcc	aat	acc	acc	ata	gag	gat	gaa	gac	gct	aaa	gcc	1152				
Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala					
		370				375					380									
ccc	agg	gtc	ccc	gac	atc	ctg	agc	tca	gtg	agg	agg	ggc	tcg	gga	gcc	1200				
Pro	Arg	Val	Pro	Asp	Ile	Leu	Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala					
385					390					395					400					
cca	gaa	gcc	gag	ggg	ccc	ctg	ccc	tgc	cca	tct	ccg	gct	ccc	ttt	agc	1248				
Pro	Glu	Ala	Glu	Gly	Pro	Leu	Pro	Cys	Pro	Ser	Pro	Ala	Pro	Phe	Ser					
				405				410						415						
ccc	ctg	cca	gcc	cca	tcc	ccc	agg	atc	tct	gac	atc	ctg	aac	tct	gtg	1296				
Pro	Leu	Pro	Ala	Pro	Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val					
			420					425					430							
aga	agg	gg	tca	gga	acc	cca	gaa	gcc	gag	ggc	ccc	ctc	tca	gcg	ggg	1344				
Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala	Glu	Gly	Pro	Leu	Ser	Ala	Gly					
		435				440						445								
ccc	ccg	ccc	tgc	ctg	tct	ccg	gct	ctc	cta	ggc	ccc	ctg	tcc	tcc	ccg	1392				
Pro	Pro	Pro	Cys	Leu	Ser	Pro	Ala	Leu	Leu	Gly	Pro	Leu	Ser	Ser	Pro					
		450				455					460									
tcc	ccc	agg	atc	tct	gac	atc	ctg	aac	tct	gtg	agg	agg	ggc	tca	ggg	1440				
Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly					
465					470					475					480					

acc cca gaa gcc gag ggc ccc tcg cca gtg ggg ccc ccg ccc tgc cca	1488
Thr Pro Glu Ala Glu Gly Pro Ser Pro Val Gly Pro Pro Pro Cys Pro	
485 490 495	
tct ccg act atc cct ggc ccc ctg ccc acc cca tcc cgg aag cag gag	1536
Ser Pro Thr Ile Pro Gly Pro Leu Pro Thr Pro Ser Arg Lys Gln Glu	
500 505 510	
atc att aag acc acg gag cag ctc atc gag gcc gtc aac aac ggt gac	1584
Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp	
515 520 525	
ttt gag gcc tac gcg aaa atc tgt gac cca ggg ctg acc tcg ttt gag	1632
Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu	
530 535 540	
cct gaa gca ctg ggc aac ctg gtt gaa ggg atg gac ttc cac aga ttc	1680
Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe	
545 550 555 560	
tac ttc gag aac ctg ctg gcc aag aac agc aag cca atc cac acg acc	1728
Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr	
565 570 575	
atc ctg aac cca cac gtg cac gtc att gga gag gat gcc gcc tgc atc	1776
Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile	
580 585 590	
gct tac atc cgg ctc acg cag tac att gac ggg cag ggc cgg ccc cgc	1824
Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg	
595 600 605	
acc agc cag tct gag gag acc cgc gtg tgg cac cgc cgc gac ggc aag	1872
Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys	
610 615 620	
tgg cag aat gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc ccg ctg	1920
Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu	
625 630 635 640	
cag	1923
Gln	

<210> 10
 <211> 641
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30

Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 35 40 45
 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 50 55 60
 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 65 70 75 80
 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 85 90 95
 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
 100 105 110
 Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His
 115 120 125
 Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
 130 135 140
 Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
 145 150 155 160
 Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
 165 170 175
 Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly
 180 185 190
 Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu
 195 200 205
 Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln
 210 215 220
 Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
 225 230 235 240
 Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn
 245 250 255
 Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val
 260 265 270
 Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val
 275 280 285
 Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile
 290 295 300
 Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala Lys Ser Leu Leu
 305 310 315 320
 Asn Lys Lys Ala Asp Gly Val Lys Pro Gln Thr Asn Ser Thr Lys Asn
 325 330 335

Ser Ala Ala Ala Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu
 340 345 350
 Glu Pro Gln Thr Thr Val Ile His Asn Pro Val Asp Gly Ile Lys Glu
 355 360 365
 Ser Ser Asp Ser Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala
 370 375 380
 Pro Arg Val Pro Asp Ile Leu Ser Ser Val Arg Arg Gly Ser Gly Ala
 385 390 395 400
 Pro Glu Ala Glu Gly Pro Leu Pro Cys Pro Ser Pro Ala Pro Phe Ser
 405 410 415
 Pro Leu Pro Ala Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val
 420 425 430
 Arg Arg Gly Ser Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly
 435 440 445
 Pro Pro Pro Cys Leu Ser Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro
 450 455 460
 Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly
 465 470 475 480
 Thr Pro Glu Ala Glu Gly Pro Ser Pro Val Gly Pro Pro Pro Cys Pro
 485 490 495
 Ser Pro Thr Ile Pro Gly Pro Leu Pro Thr Pro Ser Arg Lys Gln Glu
 500 505 510
 Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp
 515 520 525
 Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu
 530 535 540
 Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe
 545 550 555 560
 Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr
 565 570 575
 Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile
 580 585 590
 Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg
 595 600 605
 Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys
 610 615 620
 Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu
 625 630 635 640

Gln

<210> 11
 <211> 840
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(840)

```

<400> 11
atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc      48
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
   1               5               10               15

tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc      96
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
               20               25               30

aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc aag     144
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
               35               40               45

aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg atc     192
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
               50               55               60

tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc atc     240
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
               65               70               75               80

tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt ggg     288
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
               85               90               95

gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct gat     336
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
               100               105               110

gcc agt cac tgt atc cag cag atc ctg gag gcc gtt ctc cat tgt cac     384
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His
               115               120               125

caa atg ggg gtc gtc cac aga gac ctc aag ccg gag aac ctg ctt ctg     432
Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
               130               135               140

gcc agc aag tgc aaa ggg gct gca gtg aag ctg gca gac ttc ggc cta     480
Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
               145               150               155               160

gct atc gag gtg cag ggg gac cag cag gca tgg ttt ggt ttc gct ggc     528
Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
               165               170               175

```

aca cca ggc tac ctg tcc cct gag gtc ctt cgc aaa gag gcg tat ggc	576
Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly	
180 185 190	
aag cct gtg gac atc tgg gca tgt ggg gtg atc ctg tac atc ctg ctc	624
Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu	
195 200 205	
gtg ggc tac cca ccc ttc tgg gac gag gac cag cac aag ctg tac cag	672
Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln	
210 215 220	
cag atc aag gct ggt gcc tat gac ttc ccg tcc cct gag tgg gac acc	720
Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr	
225 230 235 240	
gtc act cct gaa gcc aaa aac ctc atc aac cag atg ctg acc atc aac	768
Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn	
245 250 255	
cct gcc aag cgc atc aca gcc cat gag gcc ctg aag cac ccg tgg gtc	816
Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val	
260 265 270	
tgc caa cgc tcc acg gta gca tcc	840
Cys Gln Arg Ser Thr Val Ala Ser	
275 280	
<210> 12	
<211> 280	
<212> PRT	
<213> Homo sapiens	
<400> 12	
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu	
1 5 10 15	
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val	
20 25 30	
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys	
35 40 45	
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile	
50 55 60	
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile	
65 70 75 80	
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly	
85 90 95	
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp	
100 105 110	
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His	
115 120 125	

Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
 130 135 140
 Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
 145 150 155 160
 Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
 165 170 175
 Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly
 180 185 190
 Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu
 195 200 205
 Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln
 210 215 220
 Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
 225 230 235 240
 Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn
 245 250 255
 Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val
 260 265 270
 Cys Gln Arg Ser Thr Val Ala Ser
 275 280

<210> 13
 <211> 1824
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (433) .. (1671)

<400> 13
 gcggcccgcg tgcaccgagc gcacgccgag cccgtccgcc gccgccatgg ccaccacggt 60
 gacctgcacc cgcttcaccg acgagtacca gctctacgag gatattggca agggggcttt 120
 ctctgtggtc cgacgctgtg tcaagctctg caccggccat gagtatgcag ccaagatcat 180
 caacaccaag aagctgtcag ccagagatca ccagaagctg gagagagagg ctcggatctg 240
 ccgccttggtg aagcattcca acatcgtgcg tctccacgac agcatctccg aggagggctt 300
 ccactacctg gtcttcgatc tggtcactgg tggggagctc tttgaagaca ttgtggcgag 360
 agagtactac agcgaggctg atgccagtca ctgtatccag cagatcctga ggccgttctc 420
 cattgtcacc aa atg ggg gtc gtc cac aga gac ctc aag ccg gag aac ctg 471
 Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu

1															5															10															
ctt	ctg	gcc	agc	aag	tgc	aaa	ggg	gct	gca	gtg	aag	ctg	gca	gac	ttc	519																													
Leu	Leu	Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe																														
15					20					25																																			
ggc	cta	gct	atc	gag	gtg	cag	ggg	gac	cag	cag	gca	tgg	ttt	ggg	ttc	567																													
Gly	Leu	Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe																														
30			35			40			45																																				
gct	ggc	aca	cca	ggc	tac	ctg	tcc	cct	gag	gtc	ctt	cgc	aaa	gag	gcg	615																													
Ala	Gly	Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala																														
50					55					60																																			
tac	ggc	aag	ccc	gtg	gac	atc	tgg	gca	tgt	ggg	gtg	atc	ctg	tac	atc	663																													
Tyr	Gly	Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile																														
65					70					75																																			
ctg	ctc	gtg	ggc	tac	cca	ccc	ttc	tgg	gac	gag	gac	cag	cac	aag	ctg	711																													
Leu	Leu	Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu																														
80			85					90																																					
tac	cag	cag	atc	aag	gct	ggg	gcc	tat	gac	ttc	ccg	tcc	cct	gag	tgg	759																													
Tyr	Gln	Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp																														
95			100					105																																					
gac	acc	gtc	act	cct	gaa	gcc	aaa	aac	ctc	atc	aac	cag	atg	ctg	acc	807																													
Asp	Thr	Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr																														
110		115					120					125																																	
atc	aac	cct	gcc	aag	cgc	atc	aca	gcc	cat	gag	gcc	ctg	aag	cac	ccg	855																													
Ile	Asn	Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro																														
130					135					140																																			
tgg	gtc	tgc	caa	cgc	tcc	acg	gta	gca	tcc	atg	atg	cac	aga	cag	gag	903																													
Trp	Val	Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu																														
145			150					155																																					
act	gtg	gag	tgt	ctg	aaa	aag	ttc	aat	gcc	agg	aga	aag	ctc	aag	gga	951																													
Thr	Val	Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly																														
160			165					170																																					
gcc	atc	ctc	acc	acc	atg	ctg	gcc	aca	cgg	aat	ttc	tca	gtg	ggc	aga	999																													
Ala	Ile	Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg																														
175			180					185																																					
cag	acc	acc	gct	ccg	gcc	aca	atg	tcc	acc	gcg	gcc	tcc	ggc	acc	acc	1047																													
Gln	Thr	Thr	Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr																														
190		195					200					205																																	
atg	ggg	ctg	gtg	gaa	caa	gcc	aag	agt	tta	ctc	aac	aag	aaa	gca	gat	1095																													
Met	Gly	Leu	Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp																														
210					215					220																																			
gga	gtc	aag	ccc	cag	acg	aat	agt	acc	aaa	aac	agt	gca	gcc	gcc	acc	1143																													
Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr																														
225			230					235																																					

```

agc ccc aaa ggg acg ctt cct cct gcc gcc ctg gag cct caa acc acc 1191
Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu Glu Pro Gln Thr Thr
      240                245                250

gtc atc cat aac cca gtg gac ggg att aag gag tct tct gac agt gcc 1239
Val Ile His Asn Pro Val Asp Gly Ile Lys Glu Ser Ser Asp Ser Ala
      255                260                265

aat acc acc ata gag gat gaa gac gct aaa gcc cgg aag cag gag atc 1287
Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala Arg Lys Gln Glu Ile
      270                275                280                285

att aag acc acg gag cag ctc atc gag gcc gtc aac aac ggt gac ttt 1335
Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe
      290                295                300

gag gcc tac gcg aaa atc tgt gac cca ggg ctg acc tcg ttt gag cct 1383
Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro
      305                310                315

gaa gca ctg ggc aac ctg gtt gaa ggg atg gac ttc cac aga ttc tac 1431
Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr
      320                325                330

ttc gag aac ctg ctg gcc aag aac agc aag ccg atc cac acg acc atc 1479
Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile
      335                340                345

ctg aac cca cac gtg cac gtc att gga gag gat gcc gcc tgc atc gct 1527
Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala
      350                355                360                365

tac atc cgg ctc acg cag tac att gac ggg cag ggc cgg ccc cgc acc 1575
Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr
      370                375                380

agc cag tct gag gag acc cgc gtg tgg cac cgc cgc gac ggc aag tgg 1623
Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp
      385                390                395

cag aac gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc ccg ctg cag 1671
Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
      400                405                410

tgaagagctg cgccctgggtt tcgccggaca gagttgggtgt ttggagcccg actgccctcg 1731

ggcacacggc ctgcctgtcg catgtttgtg tctgcctegt tccctccctt ggttccctgtg 1791

tctgcagaaa aacaagacca gatgtgattt gtt 1824

```

```

<210> 14
<211> 413
<212> PRT
<213> Homo sapiens

```

```

<400> 14

```

Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Ala	1	5	10	15
Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	20	25	30	
Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly	Thr	35	40	45	
Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly	Lys	50	55	60	
Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	Val	65	70	75	80
Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln	Gln	85	90	95	
Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr	Val	100	105	110	
Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	115	120	125	
Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val	Cys	130	135	140	
Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	Glu	145	150	155	160
Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	165	170	175	
Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg	Gln	Thr	Thr	180	185	190	
Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr	Met	Gly	Leu	195	200	205	
Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	210	215	220	
Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	225	230	235	240
Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile	His	245	250	255	
Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	260	265	270	
Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Arg	Lys	Gln	Glu	Ile	Ile	Lys	Thr	275	280	285	
Thr	Glu	Gln	Leu	Ile	Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	Ala	Tyr	290	295	300	

Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu
305 310 315 320

Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn
325 330 335

Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro
340 345 350

His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg
355 360 365

Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser
370 375 380

Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val
385 390 395 400

His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln
405 410

<210> 15
<211> 1676
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (25)..(1533)

<400> 15
tcgccgagcc cgtccgccgc cgcc atg gcc acc acg gtg acc tgc acc cgc 51
Met Ala Thr Thr Val Thr Cys Thr Arg
1 5

ttc acc gac gag tac cag ctc tac gag gat att ggc aag ggg gct ttc 99
Phe Thr Asp Glu Tyr Gln Leu Tyr Glu Asp Ile Gly Lys Gly Ala Phe
10 15 20 25

tct gtg gtc cga cgc tgt gtc aag ctc tgc acc ggc cat gag tat gca 147
Ser Val Val Arg Arg Cys Val Lys Leu Cys Thr Gly His Glu Tyr Ala
30 35 40

gcc aag atc atc aac acc aag aag ctg tca gcc aga gat cac cag aag 195
Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys
45 50 55

ctg gag aga gag gct cgg atc tgc cgc ctt ctg aag cat tcc aac atc 243
Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Ser Asn Ile
60 65 70

gtg cgt ctc cac gac agc atc tcc gag gag ggc ttc cac tac ctg gtc 291
Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val
75 80 85

ttc gat ctg gtc act ggt ggg gag ctc ttt gaa gac att gtg gcg aga 339
Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg

90	95	100	105	
gag tac tac agc	gag gct gat gcc agt	cac tgt atc cag cag atc	ctg	387
Glu Tyr Tyr Ser	Glu Ala Asp Ala Ser	His Cys Ile Gln Gln Ile	Leu	
	110	115	120	
gag gcc gtt ctc	cat tgt cac caa atg	ggg gtc gtc cac aga	gac ctc	435
Glu Ala Val Leu	His Cys His Gln Met	Gly Val Val His Arg	Asp Leu	
	125	130	135	
aag ccg gag aac	ctg ctt ctg gcc agc	aag tgc aaa ggg gct	gca gtg	483
Lys Pro Glu Asn	Leu Leu Leu Ala Ser	Lys Cys Lys Gly Ala	Ala Val	
	140	145	150	
aag ctg gca gac	ttc ggc cta gct atc	gag gtg cag ggg gac	cag cag	531
Lys Leu Ala Asp	Phe Gly Leu Ala Ile	Glu Val Gln Gly Asp	Gln Gln	
	155	160	165	
gca tgg ttt ggt	ttc gct ggc aca cca	ggc tac ctg tcc cct	gag gtc	579
Ala Trp Phe Gly	Phe Ala Gly Thr Pro	Gly Tyr Leu Ser Pro	Glu Val	
	170	175	180	185
ctt cgc aaa gag	gcg tac ggc aag ccc	gtg gac atc tgg gca	tgt ggg	627
Leu Arg Lys Glu	Ala Tyr Gly Lys Pro	Val Asp Ile Trp Ala	Cys Gly	
	190	195	200	
gtg atc ctg tac	atc ctg ctc gtg ggc	tac cca ccc ttc tgg	gac gag	675
Val Ile Leu Tyr	Ile Leu Leu Val Gly	Tyr Pro Pro Phe Trp	Asp Glu	
	205	210	215	
gac cag cac aag	ctg tac cag cag atc	aag gct ggt gcc tat	gac ttc	723
Asp Gln His Lys	Leu Tyr Gln Gln Ile	Lys Ala Gly Ala Tyr	Asp Phe	
	220	225	230	
ccg tcc cct gag	tgg gac acc gtc act	cct gaa gcc aaa aac	ctc atc	771
Pro Ser Pro Glu	Trp Asp Thr Val Thr	Pro Glu Ala Lys Asn	Leu Ile	
	235	240	245	
aac cag atg ctg	acc atc aac cct gcc	aag cgc atc aca gcc	cat gag	819
Asn Gln Met Leu	Thr Ile Asn Pro Ala	Lys Arg Ile Thr Ala	His Glu	
	250	255	260	265
gcc ctg aag cac	ccg tgg gtc tgc caa	cgc tcc acg gta gca	tcc atg	867
Ala Leu Lys His	Pro Trp Val Cys Gln	Arg Ser Thr Val Ala	Ser Met	
	270	275	280	
atg cac aga cag	gag act gtg gag tgt	ctg aaa aag ttc aat	gcc agg	915
Met His Arg Gln	Glu Thr Val Glu Cys	Leu Lys Lys Phe Asn	Ala Arg	
	285	290	295	
aga aag ctc aag	gga gcc atc ctc acc	acc atg ctg gcc aca	cgg aat	963
Arg Lys Leu Lys	Gly Ala Ile Leu Thr	Thr Met Leu Ala Thr	Arg Asn	
	300	305	310	
ttc tca gca gcc	aag agt tta ctc aac	aag aaa gca gat gga	gtc aag	1011
Phe Ser Ala Ala	Lys Ser Leu Leu Asn	Lys Lys Ala Asp Gly	Val Lys	
	315	320	325	

ccc cat acg aat agc acc aaa aac agt gca gcc gcc acc agc ccc aaa	1059
Pro His Thr Asn Ser Thr Lys Asn Ser Ala Ala Ala Thr Ser Pro Lys	
330 335 340 345	
ggg acg ctt cct cct gcc gcc ctg gag tct tct gac agt gcc aat acc	1107
Gly Thr Leu Pro Pro Ala Ala Leu Glu Ser Ser Asp Ser Ala Asn Thr	
350 355 360	
acc ata gag gat gaa gac gct aaa gcc cgg aag cag gag atc att aag	1155
Thr Ile Glu Asp Glu Asp Ala Lys Ala Arg Lys Gln Glu Ile Ile Lys	
365 370 375	
acc acg gag cag ctc atc gag gcc gtc aac aac ggt gac ttt gag gcc	1203
Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn Gly Asp Phe Glu Ala	
380 385 390	
tac gcg aaa atc tgt gac cca ggg ctg acc tcg ttt gag cct gaa gca	1251
Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala	
395 400 405	
ctg ggc aac ctg gtt gaa ggg atg gac ttc cac aga ttc tac ttc gag	1299
Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe Glu	
410 415 420 425	
aac ctg ctg gcc aag aac agc aag ccg atc cac acg acc atc ctg aac	1347
Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His Thr Thr Ile Leu Asn	
430 435 440	
cca cac gtg cac gtc att gga gag gat gcc gcc tgc atc gct tac atc	1395
Pro His Val His Val Ile Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile	
445 450 455	
cgg ctc acg cag tac att gac ggg cag ggc cgg ccc cgc acc agc cag	1443
Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln	
460 465 470	
tct gag gag acc cgc gtg tgg cac cgc cgc gac ggc aag tgg cag aac	1491
Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn	
475 480 485	
gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc ccg ctg cag	1533
Val His Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln	
490 495 500	
tgaagagctg cgccctgggtt tcgccggaca gagttggtgt ttggagcccg actgccctcg	1593
ggcacacggc ctgcctgtcg catgtttgtg tctgcctcgt tccctcccct ggtgcctgtg	1653
tctgcagaaa aacaagcccg act	1676

<210> 16

<211> 503

<212> PRT

<213> Homo sapiens

<400> 16

Met	Ala	Thr	Thr	Val	Thr	Cys	Thr	Arg	Phe	Thr	Asp	Glu	Tyr	Gln	Leu	1	5	10	15
Tyr	Glu	Asp	Ile	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	Arg	Arg	Cys	Val	20	25	30	
Lys	Leu	Cys	Thr	Gly	His	Glu	Tyr	Ala	Ala	Lys	Ile	Ile	Asn	Thr	Lys	35	40	45	
Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile	50	55	60	
Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile	65	70	75	80
Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly	85	90	95	
Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp	100	105	110	
Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His	115	120	125	
Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu	130	135	140	
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu	145	150	155	160
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly	165	170	175	
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly	180	185	190	
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	195	200	205	
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln	210	215	220	
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr	225	230	235	240
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	245	250	255	
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val	260	265	270	
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	275	280	285	
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	290	295	300	

Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala Ala Lys Ser Leu
 305 310 315 320
 Leu Asn Lys Lys Ala Asp Gly Val Lys Pro His Thr Asn Ser Thr Lys
 325 330 335
 Asn Ser Ala Ala Ala Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala
 340 345 350
 Leu Glu Ser Ser Asp Ser Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala
 355 360 365
 Lys Ala Arg Lys Lys Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu
 370 375 380
 Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro
 385 390 395 400
 Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly
 405 410 415
 Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser
 420 425 430
 Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His Val Ile Gly
 435 440 445
 Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp
 450 455 460
 Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val Trp
 465 470 475 480
 His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe His Cys Ser Gly
 485 490 495
 Ala Pro Val Ala Pro Leu Gln
 500

<210> 17
 <211> 2251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2088)

<400> 17
 atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc 48
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15
 tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc 96
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30

aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc aag	144
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys	
35 40 45	
aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg atc	192
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile	
50 55 60	
tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc atc	240
Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile	
65 70 75 80	
tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt ggg	288
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly	
85 90 95	
gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct gat	336
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp	
100 105 110	
gcc agg gcc act cgc act aac cca cct gct gtt tgc cac agt cac tgt	384
Ala Arg Ala Thr Arg Thr Asn Pro Pro Ala Val Cys His Ser His Cys	
115 120 125	
atc cag cag atc ctg gag gcc gtt ctc cat tgt cac caa atg ggg gtc	432
Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His Gln Met Gly Val	
130 135 140	
gtc cac aga gac ctc aag ccg gag aac ctg ctt ctg gcc agc aag tgc	480
Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys	
145 150 155 160	
aaa ggg gct gca gtg aag ctg gca gac ttc ggc cta gct atc gag gtg	528
Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val	
165 170 175	
cag ggg gac cag cag gca tgg ttt ggt ttc gct ggc aca cca ggc tac	576
Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr	
180 185 190	
ctg tcc cct gag gtc ctt cgc aaa gag gcg tat ggc aag cct gtg gac	624
Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly Lys Pro Val Asp	
195 200 205	
atc tgg gca tgt ggg gtg atc ctg tac atc ctg ctc gtg ggc tac cca	672
Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro	
210 215 220	
ccc ttc tgg gac gag gac cag cac aag ctg tac cag cag atc aag gct	720
Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala	
225 230 235 240	
ggt gcc tat gac ttc ccg tcc cct gag tgg gac acc gtc act cct gaa	768
Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu	
245 250 255	
gcc aaa aac ctc atc aac cag atg ctg acc atc aac cct gcc aag cgc	816

Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg	
			260					265					270			
atc	aca	gcc	cat	gag	gcc	ctg	aag	cac	ccg	tgg	gtc	tgc	caa	cgc	tcc	864
Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val	Cys	Gln	Arg	Ser	
		275					280					285				
acg	gta	gca	tcc	atg	atg	cac	aga	cag	gag	act	gtg	gag	tgt	ctg	aaa	912
Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	Glu	Cys	Leu	Lys	
	290						295				300					
aag	ttc	aat	gcc	agg	aga	aag	ctc	aag	gga	gcc	atc	ctc	acc	acc	atg	960
Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met	
305						310				315					320	
ctg	gcc	aca	cgg	aat	ttc	tca	gcc	aag	agt	tta	ctc	aac	aag	aaa	gca	1008
Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	
				325					330					335		
gat	gga	gtc	aag	ccc	cag	acg	aat	agc	acc	aaa	aac	agt	gca	gcc	gcc	1056
Asp	Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	
			340					345					350			
acc	agc	ccc	aaa	ggg	acg	ctt	cct	cct	gcc	gcc	ctg	gag	cct	caa	acc	1104
Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	
		355					360					365				
acc	gtc	atc	cat	aac	cca	gtg	gac	ggg	att	aag	gag	tct	tct	gac	agt	1152
Thr	Val	Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	
	370					375					380					
gcc	aat	acc	acc	ata	gag	gat	gaa	gac	gct	aaa	gcc	ccc	agg	gtc	ccc	1200
Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Pro	Arg	Val	Pro	
385					390					395					400	
gac	atc	ctg	agc	tca	gtg	agg	agg	ggc	tcg	gga	gcc	cca	gaa	gcc	gag	1248
Asp	Ile	Leu	Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala	Pro	Glu	Ala	Glu	
				405					410					415		
ggg	ccc	ctg	ccc	tgc	cca	tct	ccg	gct	ccc	ttt	agc	ccc	ctg	cca	gcc	1296
Gly	Pro	Leu	Pro	Cys	Pro	Ser	Pro	Ala	Pro	Phe	Ser	Pro	Leu	Pro	Ala	
		420						425					430			
cca	tcc	ccc	agg	atc	tct	gac	atc	ctg	aac	tct	gtg	aga	agg	ggg	tca	1344
Pro	Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	
		435					440					445				
gga	acc	cca	gaa	gcc	gag	ggc	ccc	ctc	tca	gcg	ggg	ccc	ccg	ccc	tgc	1392
Gly	Thr	Pro	Glu	Ala	Glu	Gly	Pro	Leu	Ser	Ala	Gly	Pro	Pro	Pro	Cys	
	450					455					460					
ctg	tct	ccg	gct	ctc	cta	ggc	ccc	ctg	tcc	tcc	ccg	tcc	ccc	agg	atc	1440
Leu	Ser	Pro	Ala	Leu	Leu	Gly	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Arg	Ile	
465					470				475						480	
tct	gac	atc	ctg	aac	tct	gtg	agg	agg	ggc	tca	ggg	acc	cca	gaa	gcc	1488
Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala	

485										490					495					
gag	ggc	ccc	tcg	cca	gtg	ggg	ccc	ccg	ccc	tgc	cca	tct	ccg	act	atc	1536				
Glu	Gly	Pro	Ser	Pro	Val	Gly	Pro	Pro	Pro	Cys	Pro	Ser	Pro	Thr	Ile					
			500				505						510							
cct	ggc	ccc	ctg	ccc	acc	cca	tgg	atg	gat	gac	atc	cca	ggg	ctg	ctg	1584				
Pro	Gly	Pro	Leu	Pro	Thr	Pro	Trp	Met	Asp	Asp	Ile	Pro	Gly	Leu	Leu					
			515				520						525							
cca	ccc	cca	cct	gtg	ggg	aga	cac	cag	act	ggg	ggt	ggt	gtg	gag	ata	1632				
Pro	Pro	Pro	Pro	Val	Gly	Arg	His	Gln	Thr	Gly	Gly	Gly	Val	Glu	Ile					
			530				535						540							
ctc	tta	gag	aag	agg	ctg	ctg	ggc	cac	ggg	ctc	ggc	atg	gca	ggg	cag	1680				
Leu	Leu	Glu	Lys	Arg	Leu	Leu	Gly	His	Gly	Leu	Gly	Met	Ala	Gly	Gln					
			545				550						560							
tgg	cta	gcc	cgg	aag	cag	gag	atc	att	aag	acc	acg	gag	cag	ctc	atc	1728				
Trp	Leu	Ala	Arg	Lys	Gln	Glu	Ile	Ile	Lys	Thr	Thr	Glu	Gln	Leu	Ile					
			565				570						575							
gag	gcc	gtc	aac	aac	ggt	gac	ttt	gag	gcc	tac	gcg	aaa	atc	tgt	gac	1776				
Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	Ala	Tyr	Ala	Lys	Ile	Cys	Asp					
			580				585						590							
cca	ggg	ctg	acc	tcg	ttt	gag	cct	gaa	gca	ctg	ggc	aac	ctg	gtt	gaa	1824				
Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly	Asn	Leu	Val	Glu					
			595				600						605							
ggg	atg	gac	ttc	cac	aga	ttc	tac	ttc	gag	aac	ctg	ctg	gcc	aag	aac	1872				
Gly	Met	Asp	Phe	His	Arg	Phe	Tyr	Phe	Glu	Asn	Leu	Leu	Ala	Lys	Asn					
			610				615						620							
agc	aag	ccg	atc	cac	acg	acc	atc	ctg	aac	cca	cac	gtg	cac	gtc	att	1920				
Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	Pro	His	Val	His	Val	Ile					
			625				630						640							
gga	gag	gat	gcc	gcc	tgc	atc	gct	tac	atc	cgg	ctc	acg	cag	tac	att	1968				
Gly	Glu	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	Ile	Arg	Leu	Thr	Gln	Tyr	Ile					
			645				650						655							
gac	ggg	cag	ggc	cgg	ccc	cgc	acc	agc	cag	tct	gag	gag	acc	cgc	gtg	2016				
Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	Ser	Glu	Glu	Thr	Arg	Val					
			660				665						670							
tgg	cac	cgc	cgc	gac	ggc	aag	tgg	cag	aat	gtg	cac	ttc	cac	tgc	tcg	2064				
Trp	His	Arg	Arg	Asp	Gly	Lys	Trp	Gln	Asn	Val	His	Phe	His	Cys	Ser					
			675				680						685							
ggc	gcg	cct	gtg	gcc	ccg	ctg	cag	tgaagagctg	cgccctgggt	tcgccggaca						2118				
Gly	Ala	Pro	Val	Ala	Pro	Leu	Gln													
			690				695													
gagttggtgt ttggagcccg actgccctcg ggcacacggc ctgcctgtcg catgtttgtg 2178																				
tctgcctcgt tccctcccct ggtgcctgtg tctgcagaaa aacaagacca gatgtgattt 2238																				

gttaaaaaaaaa aaa

2251

<210> 18

<211> 696

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
1 5 10 15

Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
20 25 30

Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
35 40 45

Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
50 55 60

Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
65 70 75 80

Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
85 90 95

Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
100 105 110

Ala Arg Ala Thr Arg Thr Asn Pro Pro Ala Val Cys His Ser His Cys
115 120 125

Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His Gln Met Gly Val
130 135 140

Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
145 150 155 160

Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
165 170 175

Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr
180 185 190

Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly Lys Pro Val Asp
195 200 205

Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro
210 215 220

Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala
225 230 235 240

Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu
245 250 255

Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg
 260 265 270
 Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser
 275 280 285
 Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu Lys
 290 295 300
 Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met
 305 310 315 320
 Leu Ala Thr Arg Asn Phe Ser Ala Lys Ser Leu Leu Asn Lys Lys Ala
 325 330 335
 Asp Gly Val Lys Pro Gln Thr Asn Ser Thr Lys Asn Ser Ala Ala Ala
 340 345 350
 Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu Glu Pro Gln Thr
 355 360 365
 Thr Val Ile His Asn Pro Val Asp Gly Ile Lys Glu Ser Ser Asp Ser
 370 375 380
 Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala Pro Arg Val Pro
 385 390 395 400
 Asp Ile Leu Ser Ser Val Arg Arg Gly Ser Gly Ala Pro Glu Ala Glu
 405 410 415
 Gly Pro Leu Pro Cys Pro Ser Pro Ala Pro Phe Ser Pro Leu Pro Ala
 420 425 430
 Pro Ser Pro Arg Ile Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser
 435 440 445
 Gly Thr Pro Glu Ala Glu Gly Pro Leu Ser Ala Gly Pro Pro Pro Cys
 450 455 460
 Leu Ser Pro Ala Leu Leu Gly Pro Leu Ser Ser Pro Ser Pro Arg Ile
 465 470 475 480
 Ser Asp Ile Leu Asn Ser Val Arg Arg Gly Ser Gly Thr Pro Glu Ala
 485 490 495
 Glu Gly Pro Ser Pro Val Gly Pro Pro Pro Cys Pro Ser Pro Thr Ile
 500 505 510
 Pro Gly Pro Leu Pro Thr Pro Trp Met Asp Asp Ile Pro Gly Leu Leu
 515 520 525
 Pro Pro Pro Pro Val Gly Arg His Gln Thr Gly Gly Gly Val Glu Ile
 530 535 540
 Leu Leu Glu Lys Arg Leu Leu Gly His Gly Leu Gly Met Ala Gly Gln
 545 550 555 560

Trp Leu Ala Arg Lys Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile
 565 570 575
 Glu Ala Val Asn Asn Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp
 580 585 590
 Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu
 595 600 605
 Gly Met Asp Phe His Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn
 610 615 620
 Ser Lys Pro Ile His Thr Thr Ile Leu Asn Pro His Val His Val Ile
 625 630 635 640
 Gly Glu Asp Ala Ala Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile
 645 650 655
 Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val
 660 665 670
 Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His Phe His Cys Ser
 675 680 685
 Gly Ala Pro Val Ala Pro Leu Gln
 690 695

<210> 19
 <211> 1727
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (4) .. (1629)

<400> 19
 gcc atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag 48
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln
 1 5 10 15
 cta tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt 96
 Leu Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys
 20 25 30
 gtc aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc 144
 Val Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr
 35 40 45
 aag aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg 192
 Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg
 50 55 60
 atc tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc 240
 Ile Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser
 65 70 75

atc tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt	288
Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly	
80 85 90 95	
ggg gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct	336
Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala	
100 105 110	
gat gcc agt cac tgt atc cag cag atc ctg gag gcc gtt ctc cat tgt	384
Asp Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys	
115 120 125	
cac caa atg ggg gtc gtc cac aga gac ctc aag ccg gag aac ctg ctt	432
His Gln Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu	
130 135 140	
ctg gcc agc aag tgc aaa ggg gct gca gtg aag ctg gca gac ttc ggc	480
Leu Ala Ser Lys Cys Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly	
145 150 155	
cta gct atc gag gtg cag ggg gac cag cag gca tgg ttt ggt ttc gct	528
Leu Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala	
160 165 170 175	
ggc aca cca ggc tac ctg tcc cct gag gtc ctt cgc aaa gag gcg tat	576
Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr	
180 185 190	
ggc aag cct gtg gac atc tgg gca tgt ggg gtg atc ctg tac atc ctg	624
Gly Lys Pro Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu	
195 200 205	
ctc gtg ggc tac cca ccc ttc tgg gac gag gac cag cac aag ctg tac	672
Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr	
210 215 220	
cag cag atc aag gct ggt gcc tat gac ttc ccg tcc cct gag tgg gac	720
Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp	
225 230 235	
acc gtc act cct gaa gcc aaa aac ctc atc aac cag atg ctg acc atc	768
Thr Val Thr Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile	
240 245 250 255	
aac cct gcc aag cgc atc aca gcc cat gag gcc ctg aag cac ccg tgg	816
Asn Pro Ala Lys Arg Ile Thr Ala His Glu Ala Leu Lys His Pro Trp	
260 265 270	
gtc tgc caa cgc tcc acg gta gca tcc atg atg cac aga cag gag act	864
Val Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr	
275 280 285	
gtg gag tgt ctg aaa aag ttc aat gcc agg aga aag ctc aag gga gcc	912
Val Glu Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala	
290 295 300	
atc ctc acc acc atg ctg gcc aca cgg aat ttc tca gtg ggc aga cag	960

Ile	Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg	Gln	
305						310					315					
acc	acc	gct	ccg	gcc	aca	atg	tcc	acc	gcg	gcc	tcc	ggc	acc	acc	atg	1008
Thr	Thr	Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr	Met	
320					325					330					335	
ggg	ctg	gtg	gaa	caa	gcc	aag	agt	tta	ctc	aac	aag	aaa	gca	gat	gga	1056
Gly	Leu	Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	
				340					345					350		
gtc	aag	ccc	cag	acg	aat	agc	acc	aaa	aac	agt	gca	gcc	gcc	acc	agc	1104
Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	
			355					360					365			
ccc	aaa	ggg	acg	ctt	cct	cct	gcc	gcc	ctg	gag	cct	caa	acc	acc	gtc	1152
Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	
		370					375					380				
atc	cat	aac	cca	gtg	gac	ggg	att	aag	gag	tct	tct	gac	agt	gcc	aat	1200
Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	
	385					390					395					
acc	acc	ata	gag	gat	gaa	gac	gct	aaa	gcc	cgg	aag	cag	gag	atc	att	1248
Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Arg	Lys	Gln	Glu	Ile	Ile	
400					405					410					415	
aag	acc	acg	gag	cag	ctc	atc	gag	gcc	gtc	aac	aac	ggt	gac	ttt	gag	1296
Lys	Thr	Thr	Glu	Gln	Leu	Ile	Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	
				420					425					430		
gcc	tac	gcg	aaa	atc	tgt	gac	cca	ggg	ctg	acc	tcg	ttt	gag	cct	gaa	1344
Ala	Tyr	Ala	Lys	Ile	Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	
			435					440					445			
gca	ctg	ggc	aac	ctg	gtt	gaa	ggg	atg	gac	ttc	cac	aga	ttc	tac	ttc	1392
Ala	Leu	Gly	Asn	Leu	Val	Glu	Gly	Met	Asp	Phe	His	Arg	Phe	Tyr	Phe	
		450					455					460				
gag	aac	ctg	ctg	gcc	aag	aac	agc	aag	cca	atc	cac	acg	acc	atc	ctg	1440
Glu	Asn	Leu	Leu	Ala	Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	
	465					470					475					
aac	cca	cac	gtg	cac	gtc	att	gga	gag	gat	gtc	gcc	tgc	acc	gct	tac	1488
Asn	Pro	His	Val	His	Val	Ile	Gly	Glu	Asp	Val	Ala	Cys	Thr	Ala	Tyr	
480					485					490					495	
atc	cgg	ctc	acg	cag	tac	att	gac	ggg	cag	ggc	cgg	ccc	cgc	acc	agc	1536
Ile	Arg	Leu	Thr	Gln	Tyr	Ile	Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	
				500					505					510		
cag	tct	gag	gag	acc	cgc	gtg	tgg	cac	cgc	cgc	gac	ggc	aag	tgg	cag	1584
Gln	Ser	Glu	Glu	Thr	Arg	Val	Trp	His	Arg	Arg	Asp	Gly	Lys	Trp	Gln	
			515					520					525			
aac	gtg	cac	ttc	cac	tgc	tcg	ggc	gcg	cct	gtg	gcc	ccg	ctg	cag		1629
Asn	Val	His	Phe	His	Cys	Ser	Gly	Ala	Pro	Val	Ala	Pro	Leu	Gln		

530

535

540

tgaagagctg cgccctgggt tcgccggaca gagttggtgt ttggagcccg actgccctcg 1689

ggcacacggc ctgcctgtcg catgtttgtg tctgcctc

1727

<210> 20

<211> 542

<212> PRT

<213> Homo sapiens

<400> 20

Met	Ala	Thr	Thr	Val	Thr	Cys	Thr	Arg	Phe	Thr	Asp	Glu	Tyr	Gln	Leu
1				5					10					15	

Tyr	Glu	Asp	Ile	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	Arg	Arg	Cys	Val
			20					25					30		

Lys	Leu	Cys	Thr	Gly	His	Glu	Tyr	Ala	Ala	Lys	Ile	Ile	Asn	Thr	Lys
		35					40						45		

Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile
	50					55					60				

Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile
65					70					75					80

Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly
				85					90					95	

Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp
			100					105					110		

Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His
		115					120					125			

Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu
	130					135					140				

Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu
145					150					155					160

Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly
				165					170					175	

Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly
		180						185					190		

Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu
		195					200					205			

Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln
	210					215					220				

Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr
225					230					235					240

Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	
				245					250					255		
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val	
			260					265					270			
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	
		275					280					285				
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	
	290					295					300					
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Val	Gly	Arg	Gln	Thr	
305				310						315					320	
Thr	Ala	Pro	Ala	Thr	Met	Ser	Thr	Ala	Ala	Ser	Gly	Thr	Thr	Met	Gly	
				325					330					335		
Leu	Val	Glu	Gln	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val	
			340					345					350			
Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro	
		355					360					365				
Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile	
	370					375					380					
His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr	
385					390					395					400	
Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Arg	Lys	Gln	Glu	Ile	Ile	Lys	
				405					410					415		
Thr	Thr	Glu	Gln	Leu	Ile	Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	Ala	
			420					425					430			
Tyr	Ala	Lys	Ile	Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	
		435					440					445				
Leu	Gly	Asn	Leu	Val	Glu	Gly	Met	Asp	Phe	His	Arg	Phe	Tyr	Phe	Glu	
	450					455					460					
Asn	Leu	Leu	Ala	Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	
465					470					475					480	
Pro	His	Val	His	Val	Ile	Gly	Glu	Asp	Val	Ala	Cys	Thr	Ala	Tyr	Ile	
				485					490					495		
Arg	Leu	Thr	Gln	Tyr	Ile	Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	
			500					505					510			
Ser	Glu	Glu	Thr	Arg	Val	Trp	His	Arg	Arg	Asp	Gly	Lys	Trp	Gln	Asn	
		515					520					525				
Val	His	Phe	His	Cys	Ser	Gly	Ala	Pro	Val	Ala	Pro	Leu	Gln			
	530					535					540					

<210> 21
 <211> 1689
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1546)

<400> 21
 c atg gcc acc acg gtg acc tgc acc cgc ttc acc gac gag tac cag ctc 49
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15

tac gag gat att ggc aag ggg gct ttc tct gtg gtc cga cgc tgt gtc 97
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30

aag ctc tgc acc ggc cat gag tat gca gcc aag atc atc aac acc aag 145
 Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 35 40 45

aag ctg tca gcc aga gat cac cag aag ctg gag aga gag gct cgg atc 193
 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 50 55 60

tgc cgc ctt ctg aag cat tcc aac atc gtg cgt ctc cac gac agc atc 241
 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 65 70 75 80

tcc gag gag ggc ttc cac tac ctg gtc ttc gat ctg gtc act ggt ggg 289
 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 85 90 95

gag ctc ttt gaa gac att gtg gcg aga gag tac tac agc gag gct gat 337
 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
 100 105 110

gcc agg gcc act cgc act aac cca cct gct gtt tgc cac agt cac tgt 385
 Ala Arg Ala Thr Arg Thr Asn Pro Pro Ala Val Cys His Ser His Cys
 115 120 125

atc cag cag atc ctg gag gcc gtt ctc cat tgt cac caa atg ggg gtc 433
 Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His Gln Met Gly Val
 130 135 140

gtc cac aga gac ctc aag ccg gag aac ctg ctt ctg gcc agc aag tgc 481
 Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
 145 150 155 160

aaa ggg gct gca gtg aag ctg gca gac ttc ggc cta gct atc gag gtg 529
 Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
 165 170 175

cag ggg gac cag cag gca tgg ttt ggt ttc gct ggc aca cca ggc tac 577
 Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr
 180 185 190

ctg tcc cct gag gtc ctt cgc aaa gag gcg tac ggc aag ccc gtg gac	625
Leu Ser Pro Glu Val Leu Arg Lys Glu Ala Tyr Gly Lys Pro Val Asp	
195 200 205	
atc tgg gca tgt ggg gtg atc ctg tac atc ctg ctc gtg ggc tac cca	673
Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro	
210 215 220	
ccc ttc tgg gac gag gac cag cac aag ctg tac cag cag atc aag gct	721
Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala	
225 230 235 240	
ggg gcc tat gac ttc ccg tcc cct gag tgg gac acc gtc act cct gaa	769
Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu	
245 250 255	
gcc aaa aac ctc atc aac cag atg ctg acc atc aac cct gcc aag cgc	817
Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg	
260 265 270	
atc aca gcc cat gag gcc ctg aag cac ccg tgg gtc tgc caa cgc tcc	865
Ile Thr Ala His Glu Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser	
275 280 285	
acg gta gca tcc atg atg cac aga cag gag act gtg gag tgt ctg aaa	913
Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu Lys	
290 295 300	
aag ttc aat gcc agg aga aag ctc aag gga gcc atc ctc acc acc atg	961
Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met	
305 310 315 320	
ctg gcc aca cgg aat ttc tca gca gcc aag agt tta ctc aac aag aaa	1009
Leu Ala Thr Arg Asn Phe Ser Ala Ala Lys Ser Leu Leu Asn Lys Lys	
325 330 335	
gca gat gga gtc aag ccc cat acg aat agc acc aaa aac agt gca gcc	1057
Ala Asp Gly Val Lys Pro His Thr Asn Ser Thr Lys Asn Ser Ala Ala	
340 345 350	
gcc acc agc ccc aaa ggg acg ctt cct cct gcc gcc ctg gag tct tct	1105
Ala Thr Ser Pro Lys Gly Thr Leu Pro Pro Ala Ala Leu Glu Ser Ser	
355 360 365	
gac agt gcc aat acc acc ata gag gat gaa gac gct aaa gcc cgg aag	1153
Asp Ser Ala Asn Thr Thr Ile Glu Asp Glu Asp Ala Lys Ala Arg Lys	
370 375 380	
cag gag atc att aag acc acg gag cag ctc atc gag gcc gtc aac aac	1201
Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn	
385 390 395 400	
ggg gac ttt gag gcc tac gcg aaa atc tgt gac cca ggg ctg acc tcg	1249
Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser	
405 410 415	

ttt gag cct gaa gca ctg ggc aac ctg gtt gaa ggg atg gac ttc cac 1297
 Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His
 420 425 430

aga ttc tac ttc gag aac ctg ctg gcc aag aac agc aag ccg atc cac 1345
 Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His
 435 440 445

acg acc atc ctg aac cca cac gtg cac gtc att gga gag gat gcc gcc 1393
 Thr Thr Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala
 450 455 460

tgc atc gct tac atc cgg ctc acg cag tac att gac ggg cag ggc cgg 1441
 Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg
 465 470 475 480

ccc cgc acc agc cag tct gag gag acc cgc gtg tgg cac cgc cgc gac 1489
 Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp
 485 490 495

ggc aag tgg cag aac gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc 1537
 Gly Lys Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala
 500 505 510

ccg ctg cag tgaagagctg cgccctgggt tcgccggaca gagttggtgt 1586
 Pro Leu Gln
 515

ttggagcccg actgccctcg ggcacacggc ctgcctgtcg catgtttgtg tctgcctcgt 1646

tccctcccct ggtgcctgtg tctgcagaaa aacaagcccg act 1689

<210> 22
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
 1 5 10 15
 Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val
 20 25 30
 Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys
 35 40 45
 Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
 50 55 60
 Cys Arg Leu Leu Lys His Ser Asn Ile Val Arg Leu His Asp Ser Ile
 65 70 75 80
 Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
 85 90 95
 Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp

100					105					110					
Ala	Arg	Ala	Thr	Arg	Thr	Asn	Pro	Pro	Ala	Val	Cys	His	Ser	His	Cys
		115					120					125			
Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His	Gln	Met	Gly	Val
	130					135					140				
Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Ala	Ser	Lys	Cys
145					150					155					160
Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Ile	Glu	Val
				165					170					175	
Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly	Thr	Pro	Gly	Tyr
			180					185					190		
Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly	Lys	Pro	Val	Asp
		195					200					205			
Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	Val	Gly	Tyr	Pro
	210					215					220				
Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln	Gln	Ile	Lys	Ala
225					230					235					240
Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr	Val	Thr	Pro	Glu
				245					250					255	
Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg
			260					265					270		
Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val	Cys	Gln	Arg	Ser
		275					280					285			
Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	Glu	Cys	Leu	Lys
	290					295					300				
Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met
305					310					315					320
Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys
				325					330					335	
Ala	Asp	Gly	Val	Lys	Pro	His	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala
			340					345					350		
Ala	Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Ser	Ser
		355					360					365			
Asp	Ser	Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala	Arg	Lys
	370					375					380				
Gln	Glu	Ile	Ile	Lys	Thr	Thr	Glu	Gln	Leu	Ile	Glu	Ala	Val	Asn	Asn
385					390					395					400
Gly	Asp	Phe	Glu	Ala	Tyr	Ala	Lys	Ile	Cys	Asp	Pro	Gly	Leu	Thr	Ser

	405		410		415	
Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His						
	420		425		430	
Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His						
	435		440		445	
Thr Thr Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala						
	450		455		460	
Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg						
465		470		475		480
Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp						
	485		490		495	
Gly Lys Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala						
	500		505		510	
Pro Leu Gln						
	515					
<210> 23						
<211> 2239						
<212> DNA						
<213> Homo sapiens						
<220>						
<221> CDS						
<222> (25)..(2076)						
<400> 23						
tcgccgagcc cgtccgccgc cgcc atg gcc acc acg gtg acc tgc acc cgc						51
			Met Ala Thr Thr Val Thr Cys Thr Arg			
		1		5		
ttc acc gac gag tac cag ctc tac gag gat att ggc aag ggg gct ttc						99
Phe Thr Asp Glu Tyr Gln Leu Tyr Glu Asp Ile Gly Lys Gly Ala Phe						
10		15		20		25
tct gtg gtc cga cgc tgt gtc aag ctc tgc acc ggc cat gag tat gca						147
Ser Val Val Arg Arg Cys Val Lys Leu Cys Thr Gly His Glu Tyr Ala						
	30		35		40	
gcc aag atc atc aac acc aag aag ctg tca gcc aga gat cac cag aag						195
Ala Lys Ile Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys						
	45		50		55	
ctg gag aga gag gct cgg atc tgc cgc ctt ctg aag cat tcc aac atc						243
Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Ser Asn Ile						
	60		65		70	
gtg cgt ctc cac gac agc atc tcc gag gag ggc ttc cac tac ctg gtc						291
Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val						
	75		80		85	

ttc gat ctg gtc act ggt ggg gag ctc ttt gaa gac att gtg gcg aga	339
Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg	
90 95 100 105	
gag tac tac agc gag gct gat gcc agt cac tgt atc cag cag atc ctg	387
Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu	
110 115 120	
gag gcc gtt ctc cat tgt cac caa atg ggg gtc gtc cac aga gac ctc	435
Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg Asp Leu	
125 130 135	
aag ccg gag aac ctg ctt ctg gcc agc aag tgc aaa ggg gct gca gtg	483
Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys Lys Gly Ala Ala Val	
140 145 150	
aag ctg gca gac ttc ggc cta gct atc gag gtg cag ggg gac cag cag	531
Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln Gln	
155 160 165	
gca tgg ttt ggt ttc gct ggc aca cca ggc tac ctg tcc cct gag gtc	579
Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val	
170 175 180 185	
ctt cgc aaa gag gcg tat ggc aag cct gtg gac atc tgg gca tgt ggg	627
Leu Arg Lys Glu Ala Tyr Gly Lys Pro Val Asp Ile Trp Ala Cys Gly	
190 195 200	
gtg atc ctg tac atc ctg ctc gtg ggc tac cca ccc ttc tgg gac gag	675
Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu	
205 210 215	
gac cag cac aag ctg tac cag cag atc aag gct ggt gcc tat gac ttc	723
Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe	
220 225 230	
ccg tcc cct gag tgg gac acc gtc act cct gaa gcc aaa aac ctc atc	771
Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asn Leu Ile	
235 240 245	
aac cag atg ctg acc atc aac cct gcc aag cgc atc aca gcc cat gag	819
Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala His Glu	
250 255 260 265	
gcc ctg aag cac ccg tgg gtc tgc caa cgc tcc acg gta gca tcc atg	867
Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser Thr Val Ala Ser Met	
270 275 280	
atg cac aga cag gag act gtg gag tgt ctg aaa aag ttc aat gcc agg	915
Met His Arg Gln Glu Thr Val Glu Cys Leu Lys Lys Phe Asn Ala Arg	
285 290 295	
aga aag ctc aag gga gcc atc ctc acc acc atg ctg gcc aca cgg aat	963
Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn	
300 305 310	
ttc tca gcc aag agt tta ctc aac aag aaa gca gat gga gtc aag ccc	1011

Phe	Ser	Ala	Lys	Ser	Leu	Leu	Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro		
	315					320					325						
cag	acg	aat	agc	acc	aaa	aac	agt	gca	gcc	gcc	acc	agc	ccc	aaa	ggg	1059	
Gln	Thr	Asn	Ser	Thr	Lys	Asn	Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly		
330					335				340					345			
acg	ctt	cct	cct	gcc	gcc	ctg	gag	cct	caa	acc	acc	gtc	atc	cat	aac	1107	
Thr	Leu	Pro	Pro	Ala	Ala	Leu	Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn		
				350				355						360			
cca	gtg	gac	ggg	att	aag	gag	tct	tct	gac	agt	gcc	aat	acc	acc	ata	1155	
Pro	Val	Asp	Gly	Ile	Lys	Glu	Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile		
			365				370						375				
gag	gat	gaa	gac	gct	aaa	gcc	ccc	agg	gtc	ccc	gac	atc	ctg	agc	tca	1203	
Glu	Asp	Glu	Asp	Ala	Lys	Ala	Pro	Arg	Val	Pro	Asp	Ile	Leu	Ser	Ser		
		380					385					390					
gtg	agg	agg	ggc	tcg	gga	gcc	cca	gaa	gcc	gag	ggg	ccc	ctg	ccc	tgc	1251	
Val	Arg	Arg	Gly	Ser	Gly	Ala	Pro	Glu	Ala	Glu	Gly	Pro	Leu	Pro	Cys		
	395					400					405						
cca	tct	ccg	gct	ccc	ttt	agc	ccc	ctg	cca	gcc	cca	tcc	ccc	agg	atc	1299	
Pro	Ser	Pro	Ala	Pro	Phe	Ser	Pro	Leu	Pro	Ala	Pro	Ser	Pro	Arg	Ile		
410					415				420					425			
tct	gac	atc	ctg	aac	tct	gtg	aga	agg	ggg	tca	gga	acc	cca	gaa	gcc	1347	
Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala		
				430				435						440			
gag	ggc	ccc	ctc	tca	gcg	ggg	ccc	ccg	ccc	tgc	ctg	tct	ccg	gct	ctc	1395	
Glu	Gly	Pro	Leu	Ser	Ala	Gly	Pro	Pro	Pro	Cys	Leu	Ser	Pro	Ala	Leu		
			445				450						455				
cta	ggc	ccc	ctg	tcc	tcc	ccg	tcc	ccc	agg	atc	tct	gac	atc	ctg	aac	1443	
Leu	Gly	Pro	Leu	Ser	Ser	Pro	Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn		
		460				465						470					
tct	gtg	agg	agg	ggc	tca	ggg	acc	cca	gaa	gcc	gag	ggc	ccc	tcg	cca	1491	
Ser	Val	Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala	Glu	Gly	Pro	Ser	Pro		
	475				480					485							
gtg	ggg	ccc	ccg	ccc	tgc	cca	tct	ccg	act	atc	cct	ggc	ccc	ctg	ccc	1539	
Val	Gly	Pro	Pro	Pro	Cys	Pro	Ser	Pro	Thr	Ile	Pro	Gly	Pro	Leu	Pro		
490					495				500					505			
acc	cca	tgg	atg	gat	gac	atc	cca	ggg	ctg	ctg	cca	ccc	cca	cct	gtg	1587	
Thr	Pro	Trp	Met	Asp	Asp	Ile	Pro	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Val		
				510				515						520			
ggg	aga	cac	cag	act	ggg	ggg	ggg	gtg	gag	ata	ctc	tta	gag	aag	agg	1635	
Gly	Arg	His	Gln	Thr	Gly	Gly	Gly	Val	Glu	Ile	Leu	Leu	Glu	Lys	Arg		
			525				530						535				
ctg	ctg	ggc	cac	ggg	ctc	ggc	atg	gca	ggg	cag	tgg	cta	gcc	cgg	aag	1683	
Leu	Leu	Gly	His	Gly	Leu	Gly	Met	Ala	Gly	Gln	Trp	Leu	Ala	Arg	Lys		

540	545	550	
cag gag atc att aag acc acg gag cag ctc atc gag gcc gtc aac aac			1731
Gln Glu Ile Ile Lys Thr Thr Glu Gln Leu Ile Glu Ala Val Asn Asn			
555	560	565	
ggg gac ttt gag gcc tac gcg aaa atc tgt gac cca ggg ctg acc tcg			1779
Gly Asp Phe Glu Ala Tyr Ala Lys Ile Cys Asp Pro Gly Leu Thr Ser			
570	575	580	585
ttt gag cct gaa gca ctg ggc aac ctg gtt gaa ggg ata gac ttc cac			1827
Phe Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Ile Asp Phe His			
	590	595	600
aga ttc tac ttc gag aac ctg ctg gcc aag aac agc aag ccg atc cac			1875
Arg Phe Tyr Phe Glu Asn Leu Leu Ala Lys Asn Ser Lys Pro Ile His			
	605	610	615
acg acc atc ctg aac cca cac gtg cac gtc att gga gag gat gcc gcc			1923
Thr Thr Ile Leu Asn Pro His Val His Val Ile Gly Glu Asp Ala Ala			
	620	625	630
tgc atc gct tac atc cgg ctc acg cag tac att gac ggg cag ggc cgg			1971
Cys Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Ile Asp Gly Gln Gly Arg			
	635	640	645
ccc cgc acc agc cag tct gag gag acc cgc gtg tgg cac cgc cgc gac			2019
Pro Arg Thr Ser Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp			
	650	655	660
ggc aag tgg cag aat gtg cac ttc cac tgc tcg ggc gcg cct gtg gcc			2067
Gly Lys Trp Gln Asn Val His Phe His Cys Ser Gly Ala Pro Val Ala			
	670	675	680
ccg ctg cag tgaagagctg cgccctgggt tcgccggaca gagttggtgt			2116
Pro Leu Gln			
ttggagcccg actgccctcg ggcacacggc ctgcctgtcg catgtttgtg tctgectcgt			2176
tccctcccct ggtgcctgtg tctgcagaaa aacaagacca gatgtgattt gttaaaaaaa			2236
aaa			2239
<210> 24			
<211> 684			
<212> PRT			
<213> Homo sapiens			
<400> 24			
Met Ala Thr Thr Val Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu			
1 5 10 15			
Tyr Glu Asp Ile Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Val			
20 25 30			
Lys Leu Cys Thr Gly His Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys			

35					40					45					
Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile
50						55					60				
Cys	Arg	Leu	Leu	Lys	His	Ser	Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile
65					70					75					80
Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly
				85					90					95	
Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	Ser	Glu	Ala	Asp
			100					105					110		
Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ala	Val	Leu	His	Cys	His
		115					120					125			
Gln	Met	Gly	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu
	130					135					140				
Ala	Ser	Lys	Cys	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu
145					150					155					160
Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	Gly	Phe	Ala	Gly
				165					170					175	
Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	Glu	Ala	Tyr	Gly
			180					185					190		
Lys	Pro	Val	Asp	Ile	Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu
		195					200					205			
Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln
	210					215					220				
Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr
225					230					235					240
Val	Thr	Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn
				245					250					255	
Pro	Ala	Lys	Arg	Ile	Thr	Ala	His	Glu	Ala	Leu	Lys	His	Pro	Trp	Val
			260					265					270		
Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val
		275					280					285			
Glu	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile
	290					295					300				
Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	Lys	Ser	Leu	Leu
305					310					315					320
Asn	Lys	Lys	Ala	Asp	Gly	Val	Lys	Pro	Gln	Thr	Asn	Ser	Thr	Lys	Asn
				325					330					335	
Ser	Ala	Ala	Ala	Thr	Ser	Pro	Lys	Gly	Thr	Leu	Pro	Pro	Ala	Ala	Leu

340						345						350					
Glu	Pro	Gln	Thr	Thr	Val	Ile	His	Asn	Pro	Val	Asp	Gly	Ile	Lys	Glu		
355						360						365					
Ser	Ser	Asp	Ser	Ala	Asn	Thr	Thr	Ile	Glu	Asp	Glu	Asp	Ala	Lys	Ala		
370						375						380					
Pro	Arg	Val	Pro	Asp	Ile	Leu	Ser	Ser	Val	Arg	Arg	Gly	Ser	Gly	Ala		
385						390						395					
Pro	Glu	Ala	Glu	Gly	Pro	Leu	Pro	Cys	Pro	Ser	Pro	Ala	Pro	Phe	Ser		
405						410						415					
Pro	Leu	Pro	Ala	Pro	Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val		
420						425						430					
Arg	Arg	Gly	Ser	Gly	Thr	Pro	Glu	Ala	Glu	Gly	Pro	Leu	Ser	Ala	Gly		
435						440						445					
Pro	Pro	Pro	Cys	Leu	Ser	Pro	Ala	Leu	Leu	Gly	Pro	Leu	Ser	Ser	Pro		
450						455						460					
Ser	Pro	Arg	Ile	Ser	Asp	Ile	Leu	Asn	Ser	Val	Arg	Arg	Gly	Ser	Gly		
465						470						475					
Thr	Pro	Glu	Ala	Glu	Gly	Pro	Ser	Pro	Val	Gly	Pro	Pro	Pro	Cys	Pro		
485						490						495					
Ser	Pro	Thr	Ile	Pro	Gly	Pro	Leu	Pro	Thr	Pro	Trp	Met	Asp	Asp	Ile		
500						505						510					
Pro	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Val	Gly	Arg	His	Gln	Thr	Gly	Gly		
515						520						525					
Gly	Val	Glu	Ile	Leu	Leu	Glu	Lys	Arg	Leu	Leu	Gly	His	Gly	Leu	Gly		
530						535						540					
Met	Ala	Gly	Gln	Trp	Leu	Ala	Arg	Lys	Gln	Glu	Ile	Ile	Lys	Thr	Thr		
545						550						555					
Glu	Gln	Leu	Ile	Glu	Ala	Val	Asn	Asn	Gly	Asp	Phe	Glu	Ala	Tyr	Ala		
565						570						575					
Lys	Ile	Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly		
580						585						590					
Asn	Leu	Val	Glu	Gly	Ile	Asp	Phe	His	Arg	Phe	Tyr	Phe	Glu	Asn	Leu		
595						600						605					
Leu	Ala	Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	Pro	His		
610						615						620					
Val	His	Val	Ile	Gly	Glu	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	Ile	Arg	Leu		
625						630						635					
Thr	Gln	Tyr	Ile	Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	Ser	Glu		

	645		650		655	
Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln Asn Val His						
	660		665		670	
Phe His Cys Ser Gly Ala Pro Val Ala Pro Leu Gln						
	675		680			

<210> 25
 <211> 3309
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (295) .. (1983)

 <400> 25
 gcggccgcgc tgccctggcag cccgggaagc cgcggcacag ctgctcggcg cctgcagctc 60
 cggctcgggg gctggaaccg aagcgggggc ggccgggagcg cggagaccac agccccggg 120
 gagaggcgga gggggtcctt ggccctgggcg gagaggctga gctgagtgcg cgtgagaaag 180
 agggctgcac cgctgctcgg cgcggactct gccagcccca gcttcagccc cggctcaggt 240
 cgccgcagcc cgggagcctc cccgcttgcg cccaaggca cgcgcggcac agcc atg 297
 Met
 1

 aac acc aac gat gcc aag gag tat ctg gcc cgg agg gaa atc cct cag 345
 Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg Arg Glu Ile Pro Gln
 5 10 15

 ctt ttt gag agc ctt ttg aat gga ctg atg tgt tct aag ccc gaa gat 393
 Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys Ser Lys Pro Glu Asp
 20 25 30

 cca gta gaa tac ttg gaa agt tgt tta caa aaa gta aag gaa ctg ggt 441
 Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys Val Lys Glu Leu Gly
 35 40 45

 ggc tgt gac aag gtg aaa tgg gat aca ttt gta agc cag gaa aag aag 489
 Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val Ser Gln Glu Lys Lys
 50 55 60 65

 acc tta cct cca cta aat gga gga cag tca cgg aga tcc ttt cta aga 537
 Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg Arg Ser Phe Leu Arg
 70 75 80

 aat gta atg cct gaa aac tca aac ttt cca tat cgg cgg tat gac cgg 585
 Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr Arg Arg Tyr Asp Arg
 85 90 95

 ctc cct cca atc cat caa ttc tcc ata gaa agt gac acg gat ctc tct 633
 Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser Asp Thr Asp Leu Ser
 100 105 110

gag act gca gag ttg att gag gag tat gag gtt ttt gat cct acc aga	681
Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr Arg	
115 120 125	
cct cga cca aaa atc att ctt gtt ata ggt ggt cca gga agt gga aag	729
Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly Lys	
130 135 140 145	
ggg act cag agt ttg aaa att gca gaa cga tat gga ttc caa tac att	777
Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile	
150 155 160	
tct gtg gga gaa tta tta aga aag aag atc cac agt acc agc agc aat	825
Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser Asn	
165 170 175	
agg aaa tgg agt ctt att gcc aag ata att aca act gga gaa ttg gcc	873
Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu Ala	
180 185 190	
cca cag gaa aca aca att aca gag ata aaa caa aaa ttg atg caa ata	921
Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln Ile	
195 200 205	
cct gat gaa gag ggc att gtt att gat gga ttt cca aga gat gtt gcc	969
Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe Pro Arg Asp Val Ala	
210 215 220 225	
cag gct cta tct ttt gag gac caa atc tgt acc ccc gat ttt gtg gta	1017
Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr Pro Asp Phe Val Val	
230 235 240	
ttc ctg gct tgt gct aat cag aga ctc aaa gaa aga tta ctg aag cgt	1065
Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys Glu Arg Leu Leu Lys Arg	
245 250 255	
gca gaa cag cag ggc cga cca gac gac aat gta aaa gct acc caa agg	1113
Ala Glu Gln Gln Gly Arg Pro Asp Asp Asn Val Lys Ala Thr Gln Arg	
260 265 270	
aga cta atg aac ttc aag cag aat gct gct cca ttg gtt aaa tac ttc	1161
Arg Leu Met Asn Phe Lys Gln Asn Ala Ala Pro Leu Val Lys Tyr Phe	
275 280 285	
cag gaa aag ggg ctc atc atg aca ttt gat gcc gac cgc gat gag gat	1209
Gln Glu Lys Gly Leu Ile Met Thr Phe Asp Ala Asp Arg Asp Glu Asp	
290 295 300 305	
gag gtg ttc tat gac atc agc atg gca gtt gac aac aag tta ttt cca	1257
Glu Val Phe Tyr Asp Ile Ser Met Ala Val Asp Asn Lys Leu Phe Pro	
310 315 320	
aac aaa gag gct gca gca ggt tca agt gac ctt gat cct tcg atg ata	1305
Asn Lys Glu Ala Ala Ala Gly Ser Ser Asp Leu Asp Pro Ser Met Ile	
325 330 335	

ttg gac act gga gag atc att gat aca gga tct gat tat gaa gat cag	1353
Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp Gln	
340 345 350	
ggt gat gac cag tta aat gta ttt gga gag gac act atg gga ggt ttc	1401
Gly Asp Asp Gln Leu Asn Val Phe Gly Glu Asp Thr Met Gly Gly Phe	
355 360 365	
atg gaa gat ttg aga aag tgt aaa att att ttc ata att ggt ggt cct	1449
Met Glu Asp Leu Arg Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly Pro	
370 375 380 385	
ggc tct ggc aaa ggc aca cag tgt gaa aag ctg gtg gaa aaa tat gga	1497
Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr Gly	
390 395 400	
ttt aca cat ctc tca act ggc gag ctc ctg cgt gag gaa ctg gca tca	1545
Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala Ser	
405 410 415	
gaa tct gaa aga agc aaa ttg atc aga gac att atg gaa cgt gga gac	1593
Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp Ile Met Glu Arg Gly Asp	
420 425 430	
ctg gtg ccc tca ggc atc gtt ttg gag ctc ctg aag gag gcc atg gtg	1641
Leu Val Pro Ser Gly Ile Val Leu Glu Leu Leu Lys Glu Ala Met Val	
435 440 445	
gcc agc ctc ggg gac acc agg ggc ttc ctg att gac ggc tat cct cgg	1689
Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp Gly Tyr Pro Arg	
450 455 460 465	
gag gtg aag caa ggg gaa gag ttc gga cgc agg att gga gac cca cag	1737
Glu Val Lys Gln Gly Glu Glu Phe Gly Arg Arg Ile Gly Asp Pro Gln	
470 475 480	
ttg gtg atc tgt atg gac tgc tcg gca gac acc atg acc aac cgc ctt	1785
Leu Val Ile Cys Met Asp Cys Ser Ala Asp Thr Met Thr Asn Arg Leu	
485 490 495	
ctc caa agg agc cgg agc agc ctg cct gtg gac gac acc acc aag acc	1833
Leu Gln Arg Ser Arg Ser Ser Leu Pro Val Asp Asp Thr Thr Lys Thr	
500 505 510	
atc gcc aag cgc cta gaa gcc tac tac cga gcg tcc atc ccc gtg atc	1881
Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg Ala Ser Ile Pro Val Ile	
515 520 525	
gcc tac tac gag aca aaa aca cag cta cac aag ata aat gca gag gga	1929
Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His Lys Ile Asn Ala Glu Gly	
530 535 540 545	
aca cca gag gac gtt ttt ctt caa ctc tgc aca gct att gac tct att	1977
Thr Pro Glu Asp Val Phe Leu Gln Leu Cys Thr Ala Ile Asp Ser Ile	
550 555 560	
att ttc tgaaggcaaa aatgcatggt. tgtagaatg gaaacagaaa aacattaaaa	2033

Ile Phe

```
agttcattcc ttaacacaat gtttcaagtt aaaccttttg tgtcaccgcc cccaccaaac 2093
caccacctcc taaatcctga cagcactggt tgcttcccag ctagacctgt gtgagaggtg 2153
tctggaaatc atgcatggtg tatttgggac tatatcaacc tattctccac acttcagaca 2213
actgtctgca ctcacggcac gcacactttg tatcatgcag gccacactca gagctagtca 2273
gtacatgaac agtgggtgagg tgccagtctg tgtccgttgt gatcacagga cttgctagac 2333
cctgatcatc tggttctcct ctcatgaagc atccctaacc cccagtcaca ccttctctct 2393
acatactggt cccaatgga ggccctggc ataggggaca gccctgggca tcttctcttg 2453
gtgtctggct gttttgtcaa ctctcatcca ctgggtggctc agagccataa ggtggggtga 2513
ttacacaatg cttgtacat gatatagagg catcaagcaa gtaaaatttg acagaaattt 2573
taaaatatga agatgtatag ctttcccaag atgatggtaa aaccagggtt agtcatcagt 2633
aaccttctct attattatta ttttttagaa acttgaata ctgtcattat ggctaagaga 2693
acaaatctga taaattgtgt aacctagtct cttctctaca tggatgatga tttcagcaat 2753
tataaattaa tataaatgac caaaagtaac ttaaaagcat gagatatttg ctatttcatt 2813
cattgggcac atatcaaatt ataattttga ttttaaagg tcacccatgt atttggtgcc 2873
aagcaagtaa aaaaataccc taacaaacct gatgtgggtg ggagggggcat gtcagtaagt 2933
ggtgtgttca atgtgtttgt ttcatatggg ccctttccag gagtttgcaa acctgtcat 2993
acccatatgc aaaactgtgt ttccttgcat taaaccagtg aagtttgggt tctcttttgt 3053
gctatcaatc agttgtaaaa tcagagcttc ttatatattc tactggaata actgcatctt 3113
ccactcagtc actacaaaaa agcatagttt cagtttgcat gaattttttt tttttcttc 3173
aatggttgtg cagataagga tccatttctg ggatagaatt gtatttttta agtcattttt 3233
tttcttgaa atggatatgt acaataaaaa ttaaatggaa gacaggaaaa aaaaaaaaaa 3293
aaaaaaaaa aaaaaa 3309
```

<210> 26

<211> 563

<212> PRT

<213> Homo sapiens

<400> 26

Met	Asn	Thr	Asn	Asp	Ala	Lys	Glu	Tyr	Leu	Ala	Arg	Arg	Glu	Ile	Pro
1				5					10					15	

Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys Ser Lys Pro Glu

20					25					30						
Asp	Pro	Val	Glu	Tyr	Leu	Glu	Ser	Cys	Leu	Gln	Lys	Val	Lys	Glu	Leu	
35					40					45						
Gly	Gly	Cys	Asp	Lys	Val	Lys	Trp	Asp	Thr	Phe	Val	Ser	Gln	Glu	Lys	
50					55					60						
Lys	Thr	Leu	Pro	Pro	Leu	Asn	Gly	Gly	Gln	Ser	Arg	Arg	Ser	Phe	Leu	
65					70					75					80	
Arg	Asn	Val	Met	Pro	Glu	Asn	Ser	Asn	Phe	Pro	Tyr	Arg	Arg	Tyr	Asp	
85					90					95						
Arg	Leu	Pro	Pro	Ile	His	Gln	Phe	Ser	Ile	Glu	Ser	Asp	Thr	Asp	Leu	
100					105					110						
Ser	Glu	Thr	Ala	Glu	Leu	Ile	Glu	Glu	Tyr	Glu	Val	Phe	Asp	Pro	Thr	
115					120					125						
Arg	Pro	Arg	Pro	Lys	Ile	Ile	Leu	Val	Ile	Gly	Gly	Pro	Gly	Ser	Gly	
130					135					140						
Lys	Gly	Thr	Gln	Ser	Leu	Lys	Ile	Ala	Glu	Arg	Tyr	Gly	Phe	Gln	Tyr	
145					150					155					160	
Ile	Ser	Val	Gly	Glu	Leu	Leu	Arg	Lys	Lys	Ile	His	Ser	Thr	Ser	Ser	
165					170					175						
Asn	Arg	Lys	Trp	Ser	Leu	Ile	Ala	Lys	Ile	Ile	Thr	Thr	Gly	Glu	Leu	
180					185					190						
Ala	Pro	Gln	Glu	Thr	Thr	Ile	Thr	Glu	Ile	Lys	Gln	Lys	Leu	Met	Gln	
195					200					205						
Ile	Pro	Asp	Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val	
210					215					220						
Ala	Gln	Ala	Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Phe	Val	
225					230					235					240	
Val	Phe	Leu	Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys	
245					250					255						
Arg	Ala	Glu	Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln	
260					265					270						
Arg	Arg	Leu	Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr	
275					280					285						
Phe	Gln	Glu	Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp	Ala	Asp	Arg	Asp	Glu	
290					295					300						
Asp	Glu	Val	Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val	Asp	Asn	Lys	Leu	Phe	
305					310					315					320	
Pro	Asn	Lys	Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ser	Met	

c acc aga tct ata att ggt ggt cct ggc tct ggc aaa ggc aca cag tgt 49
Thr Arg Ser Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys
1 5 10 15
gaa aag ctg gtg gaa aaa tat gga ttt aca cat ctc tca act ggc gag 97
Glu Lys Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu
20 25 30
ctc ctg cgt gag gaa ctg gca tca gaa tct gaa aga agc aaa ttg atc 145
Leu Leu Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile
35 40 45
aga gac att atg gaa cgt gga gac ctg gtg ccc tca ggc atc gtt ttg 193
Arg Asp Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Leu
50 55 60
gag ctg ctg aag gag gcc atg gtg gcc agc ctc ggg gac acc agg ggc 241
Glu Leu Leu Lys Glu Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly
65 70 75 80
ttc ctg att gac ggc tat cct cgg gag gtg aag caa ggg gaa gag ttc 289
Phe Leu Ile Asp Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe
85 90 95
gga cgc agg att gga gac cca cag ttg gtg atc tgt atg gac tgc tcg 337
Gly Arg Arg Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser
100 105 110
gca gac acc atg acc aac cgc ctt ctc caa agg agc cgg agc agc ctg 385
Ala Asp Thr Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu
115 120 125
cct gtg gac gac acc acc aag acc atc gcc aag cgc cta gaa gcc tac 433
Pro Val Asp Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr
130 135 140
tac cga gcg tcc atc ccc gtg atc gcc tac tac gag aca aaa aca cag 481
Tyr Arg Ala Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr Gln
145 150 155 160
gtc gac ggc
Val Asp Gly 490

<210> 28
<211> 163
<212> PRT
<213> Homo sapiens

<400> 28
Thr Arg Ser Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys
1 5 10 15
Glu Lys Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu
20 25 30
Leu Leu Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile

35	40	45	
Arg Asp Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Leu			
50	55	60	
Glu Leu Leu Lys Glu Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly			
65	70	75	80
Phe Leu Ile Asp Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe			
	85	90	95
Gly Arg Arg Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser			
	100	105	110
Ala Asp Thr Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu			
	115	120	125
Pro Val Asp Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr			
	130	135	140
Tyr Arg Ala Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr Gln			
145	150	155	160
Val Asp Gly			
<210> 29			
<211> 493			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (2) .. (493)			
<400> 29			
c acc aga tct gtt ata ggt ggt cca gga agt gga aag ggt act cag agt			49
Thr Arg Ser Val Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Ser			
1	5	10	15
ttg aaa att gca gaa cga tat gga ttc caa tac att tct gtg gga gaa			97
Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile Ser Val Gly Glu			
	20	25	30
tta tta aga aag aag atc cac agt acc agc agc aat agg aaa tgg agt			145
Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser Asn Arg Lys Trp Ser			
	35	40	45
ctt att gcc aag ata att aca act gga gaa ttg gcc cca cag gaa aca			193
Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu Ala Pro Gln Glu Thr			
	50	55	60
aca att aca gag ata aaa caa aaa ttg atg caa ata cct gat gaa gag			241
Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln Ile Pro Asp Glu Glu			
65	70	75	80
ggc att gtt att gat gga ttt cca aga gat gtt gcc cag gct cta tct			289

Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val	Ala	Gln	Ala	Leu	Ser	
				85					90					95		
ttt	gag	gac	caa	atc	tgt	acc	ccc	gat	ttg	gtg	gta	ttc	ctg	gct	tgt	337
Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Leu	Val	Val	Phe	Leu	Ala	Cys	
			100					105					110			
gct	aat	cag	aga	ctc	aaa	gaa	aga	tta	ctg	aag	cgt	gca	gaa	cag	cag	385
Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys	Arg	Ala	Glu	Gln	Gln	
			115					120				125				
ggc	cga	cca	gac	gac	aat	gta	aaa	gct	acc	caa	agg	aga	cta	atg	aac	433
Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln	Arg	Arg	Leu	Met	Asn	
			130				135				140					
ttc	aag	cag	aat	gct	gct	cca	ttg	gtt	aaa	tac	ttc	cag	gaa	aag	ggg	481
Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr	Phe	Gln	Glu	Lys	Gly	
						150				155					160	
ctc	gtc	gac	ggc													493
Leu	Val	Asp	Gly													

<210> 30
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 30																
Thr	Arg	Ser	Val	Ile	Gly	Gly	Pro	Gly	Ser	Gly	Lys	Gly	Thr	Gln	Ser	
1				5					10					15		
Leu	Lys	Ile	Ala	Glu	Arg	Tyr	Gly	Phe	Gln	Tyr	Ile	Ser	Val	Gly	Glu	
			20					25					30			
Leu	Leu	Arg	Lys	Lys	Ile	His	Ser	Thr	Ser	Ser	Asn	Arg	Lys	Trp	Ser	
			35				40					45				
Leu	Ile	Ala	Lys	Ile	Ile	Thr	Thr	Gly	Glu	Leu	Ala	Pro	Gln	Glu	Thr	
			50			55					60					
Thr	Ile	Thr	Glu	Ile	Lys	Gln	Lys	Leu	Met	Gln	Ile	Pro	Asp	Glu	Glu	
			65			70				75					80	
Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val	Ala	Gln	Ala	Leu	Ser	
				85					90					95		
Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Leu	Val	Val	Phe	Leu	Ala	Cys	
			100					105					110			
Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys	Arg	Ala	Glu	Gln	Gln	
			115					120				125				
Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln	Arg	Arg	Leu	Met	Asn	
			130				135				140					
Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr	Phe	Gln	Glu	Lys	Gly	

145

150

155

160

Leu Val Asp Gly

<210> 31

<211> 1714

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(1714)

<400> 31

c acc aga tct ccc acc atg aac acc aac gat gcc aag gag tat ctg gcc 49
 Thr Arg Ser Pro Thr Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala
 1 5 10 15

cgg agg gaa atc cct cag ctt ttt gag agc ctt ttg aat gga ctg atg 97
 Arg Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met
 20 25 30

tgt tct aag ccc gaa gat cca gta gaa tac ttg gaa agt tgt tta caa 145
 Cys Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln
 35 40 45

aaa gta aag gaa ctg ggt ggc tgt gac aag gtg aaa tgg gat aca ttt 193
 Lys Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe
 50 55 60

gta agc cag gaa aag aag acc tta cct cca cta aat gga gga cag tca 241
 Val Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser
 65 70 75 80

cgg aga tcc ttt cta aga aat gta atg cct gaa aac tca aac ttt cca 289
 Arg Arg Ser Phe Leu Arg Asn Val Met Pro Glu Asn Ser Asn Phe Pro
 85 90 95

tat cgg cgg tat gac cgg ctc cct cca atc cat caa ttc tcc ata gaa 337
 Tyr Arg Arg Tyr Asp Arg Leu Pro Pro Ile His Gln Phe Ser Ile Glu
 100 105 110

agt gac acg gat ctc tct gag act gca gag ttg att gag gag tat gag 385
 Ser Asp Thr Asp Leu Ser Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu
 115 120 125

gtt ttt gat cct acc aga cct cga cca aaa atc att ctt gtt ata ggt 433
 Val Phe Asp Pro Thr Arg Pro Arg Pro Lys Ile Ile Leu Val Ile Gly
 130 135 140

ggt cca gga agt gga aag ggt act cag agt ttg aaa att gca gaa cga 481
 Gly Pro Gly Ser Gly Lys Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg
 145 150 155 160

tat gga ttc caa tac att tct gtg gga gaa tta tta aga aag aag atc 529
 Tyr Gly Phe Gln Tyr Ile Ser Val Gly Glu Leu Leu Arg Lys Lys Ile

165										170					175					
cac	agt	acc	agc	agc	aat	agg	aaa	tgg	agt	ctt	att	gcc	aag	ata	att	577				
His	Ser	Thr	Ser	Ser	Asn	Arg	Lys	Trp	Ser	Leu	Ile	Ala	Lys	Ile	Ile					
			180					185					190							
aca	act	gga	gaa	ttg	gcc	cca	cag	gaa	aca	aca	att	aca	gag	ata	aaa	625				
Thr	Thr	Gly	Glu	Leu	Ala	Pro	Gln	Glu	Thr	Thr	Ile	Thr	Glu	Ile	Lys					
		195					200					205								
caa	aaa	ttg	atg	caa	ata	cct	gat	gaa	gag	ggc	att	gtt	att	gat	gga	673				
Gln	Lys	Leu	Met	Gln	Ile	Pro	Asp	Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly					
	210					215					220									
ttt	cca	aga	gat	gtt	gcc	cag	gct	cta	tct	ttt	gag	gac	caa	atc	tgt	721				
Phe	Pro	Arg	Asp	Val	Ala	Gln	Ala	Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys					
225					230					235					240					
acc	ccc	gat	ttg	gtg	gta	ttc	ctg	gct	tgt	gct	aat	cag	aga	ctc	aaa	769				
Thr	Pro	Asp	Leu	Val	Val	Phe	Leu	Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys					
				245					250					255						
gaa	aga	tta	ctg	aag	cgt	gca	gaa	cag	cag	ggc	cga	cca	gac	gac	aat	817				
Glu	Arg	Leu	Leu	Lys	Arg	Ala	Glu	Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn					
			260					265					270							
gta	aaa	gct	acc	caa	agg	aga	cta	atg	aac	ttc	aag	cag	aat	gct	gct	865				
Val	Lys	Ala	Thr	Gln	Arg	Arg	Leu	Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala					
	275						280					285								
cca	ttg	gtt	aaa	tac	ttc	cag	gaa	aag	ggg	ctc	atc	atg	aca	ttt	gat	913				
Pro	Leu	Val	Lys	Tyr	Phe	Gln	Glu	Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp					
	290					295					300									
gcc	gac	cgc	gat	gag	gat	gag	gtg	ttc	tat	gac	atc	agc	atg	gca	gtt	961				
Ala	Asp	Arg	Asp	Glu	Asp	Glu	Val	Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val					
305					310					315					320					
gac	aac	aag	tta	ttt	cca	aac	aaa	gag	gct	gca	gca	ggt	tca	agt	gac	1009				
Asp	Asn	Lys	Leu	Phe	Pro	Asn	Lys	Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp					
				325					330					335						
ctt	gat	cct	tcg	atg	ata	ttg	gac	act	gga	gag	atc	att	gat	aca	gga	1057				
Leu	Asp	Pro	Ser	Met	Ile	Leu	Asp	Thr	Gly	Glu	Ile	Ile	Asp	Thr	Gly					
			340					345					350							
tct	gat	tat	gaa	gat	cag	ggt	gat	gac	cag	tta	aat	gta	ttt	gga	gag	1105				
Ser	Asp	Tyr	Glu	Asp	Gln	Gly	Asp	Asp	Gln	Leu	Asn	Val	Phe	Gly	Glu					
		355					360					365								
gac	act	atg	gga	ggt	ttc	atg	gaa	gat	ttg	aga	aag	tgt	aaa	att	att	1153				
Asp	Thr	Met	Gly	Gly	Phe	Met	Glu	Asp	Leu	Arg	Lys	Cys	Lys	Ile	Ile					
	370					375					380									
ttc	ata	att	ggt	ggt	cct	ggc	tct	ggc	aaa	ggc	aca	cag	tgt	gaa	aag	1201				
Phe	Ile	Ile	Gly	Gly	Pro	Gly	Ser	Gly	Lys	Gly	Thr	Gln	Cys	Glu	Lys					
385					390					395					400					

ctg gtg gaa aaa tat gga ttt aca cat ctc tca act ggc gag ctc ctg	1249
Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu	
405 410 415	
cgt gag gaa ctg gca tca gaa tct gaa aga agc aaa ttg atc aga gac	1297
Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp	
420 425 430	
att atg gaa cgt gga gac ctg gtg ccc tca ggc atc gtt ttg gag ctc	1345
Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu	
435 440 445	
ctg aag gag gcc atg gtg gcc agc ctc ggg gac acc agg ggc ttc ctg	1393
Leu Lys Glu Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu	
450 455 460	
att gac ggc tat cct cgg gag gtg aag caa ggg gaa gag ttc gga cgc	1441
Ile Asp Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe Gly Arg	
465 470 475 480	
agg att gga gac cca cag ttg gtg atc tgt atg gac tgc tcg gca gac	1489
Arg Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser Ala Asp	
485 490 495	
acc atg acc aac cgc ctt ctc caa agg agc cgg agc agc ctg cct gtg	1537
Thr Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu Pro Val	
500 505 510	
gac gac acc acc aag acc atc gcc aag cgc cta gaa gcc tac tac cga	1585
Asp Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg	
515 520 525	
gcg tcc atc ccc gtg atc gcc tac tac gag aca aaa aca cag cta cac	1633
Ala Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His	
530 535 540	
aag ata aat gca gag gga aca cca gag gac gtt ttt ctt caa ctc tgc	1681
Lys Ile Asn Ala Glu Gly Thr Pro Glu Asp Val Phe Leu Gln Leu Cys	
545 550 555 560	
aca gct att gac tct att att ttc gtc gac ggc	1714
Thr Ala Ile Asp Ser Ile Ile Phe Val Asp Gly	
565 570	
<210> 32	
<211> 571	
<212> PRT	
<213> Homo sapiens	
<400> 32	
Thr Arg Ser Pro Thr Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala	
1 5 10 15	
Arg Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met	
20 25 30	

Cys	Ser	Lys	Pro	Glu	Asp	Pro	Val	Glu	Tyr	Leu	Glu	Ser	Cys	Leu	Gln	35	40	45
Lys	Val	Lys	Glu	Leu	Gly	Gly	Cys	Asp	Lys	Val	Lys	Trp	Asp	Thr	Phe	50	55	60
Val	Ser	Gln	Glu	Lys	Lys	Thr	Leu	Pro	Pro	Leu	Asn	Gly	Gly	Gln	Ser	65	70	75
Arg	Arg	Ser	Phe	Leu	Arg	Asn	Val	Met	Pro	Glu	Asn	Ser	Asn	Phe	Pro	85	90	95
Tyr	Arg	Arg	Tyr	Asp	Arg	Leu	Pro	Pro	Ile	His	Gln	Phe	Ser	Ile	Glu	100	105	110
Ser	Asp	Thr	Asp	Leu	Ser	Glu	Thr	Ala	Glu	Leu	Ile	Glu	Glu	Tyr	Glu	115	120	125
Val	Phe	Asp	Pro	Thr	Arg	Pro	Arg	Pro	Lys	Ile	Ile	Leu	Val	Ile	Gly	130	135	140
Gly	Pro	Gly	Ser	Gly	Lys	Gly	Thr	Gln	Ser	Leu	Lys	Ile	Ala	Glu	Arg	145	150	155
Tyr	Gly	Phe	Gln	Tyr	Ile	Ser	Val	Gly	Glu	Leu	Leu	Arg	Lys	Lys	Ile	165	170	175
His	Ser	Thr	Ser	Ser	Asn	Arg	Lys	Trp	Ser	Leu	Ile	Ala	Lys	Ile	Ile	180	185	190
Thr	Thr	Gly	Glu	Leu	Ala	Pro	Gln	Glu	Thr	Thr	Ile	Thr	Glu	Ile	Lys	195	200	205
Gln	Lys	Leu	Met	Gln	Ile	Pro	Asp	Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly	210	215	220
Phe	Pro	Arg	Asp	Val	Ala	Gln	Ala	Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys	225	230	235
Thr	Pro	Asp	Leu	Val	Val	Phe	Leu	Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys	245	250	255
Glu	Arg	Leu	Leu	Lys	Arg	Ala	Glu	Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn	260	265	270
Val	Lys	Ala	Thr	Gln	Arg	Arg	Leu	Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala	275	280	285
Pro	Leu	Val	Lys	Tyr	Phe	Gln	Glu	Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp	290	295	300
Ala	Asp	Arg	Asp	Glu	Asp	Glu	Val	Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val	305	310	315
Asp	Asn	Lys	Leu	Phe	Pro	Asn	Lys	Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp	325	330	335

Leu Asp Pro Ser Met Ile Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly
 340 345 350
 Ser Asp Tyr Glu Asp Gln Gly Asp Asp Gln Leu Asn Val Phe Gly Glu
 355 360 365
 Asp Thr Met Gly Gly Phe Met Glu Asp Leu Arg Lys Cys Lys Ile Ile
 370 375 380
 Phe Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys
 385 390 395 400
 Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu
 405 410 415
 Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp
 420 425 430
 Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu
 435 440 445
 Leu Lys Glu Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu
 450 455 460
 Ile Asp Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe Gly Arg
 465 470 475 480
 Arg Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser Ala Asp
 485 490 495
 Thr Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu Pro Val
 500 505 510
 Asp Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg
 515 520 525
 Ala Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His
 530 535 540
 Lys Ile Asn Ala Glu Gly Thr Pro Glu Asp Val Phe Leu Gln Leu Cys
 545 550 555 560
 Thr Ala Ile Asp Ser Ile Ile Phe Val Asp Gly
 565 570

 <210> 33
 <211> 1642
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (2) .. (1642)

 <400> 33
 c acc aga tct ccc acc atg aac acc aac gat gcc aag gag tat ctg gcc 49
 Thr Arg Ser Pro Thr Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala

1	5	10	15	
cgg agg gaa atc cct cag ctt ttt gag agc ctt ttg aat gga ctg atg	Arg Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met	97		
20	25	30		
tgt tct aag ccc gaa gat cca gta gaa tac ttg gaa agt tgt tta caa	Cys Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln	145		
35	40	45		
aaa gta aag gaa ctg ggt ggc tgt gac aag gtg aaa tgg gat aca ttt	Lys Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe	193		
50	55	60		
gta agc cag gaa aag aag acc tta cct cca cta aat gga gga cag tca	Val Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser	241		
65	70	75	80	
cgg aga tcc ttt cta aga aat gaa agt gac acg gat ctc tct gag act	Arg Arg Ser Phe Leu Arg Asn Glu Ser Asp Thr Asp Leu Ser Glu Thr	289		
85	90	95		
gca gag ttg att gag gag tat gag gtt ttt gat cct acc aga cct cga	Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr Arg Pro Arg	337		
100	105	110		
cca aaa atc att ctt gtt ata ggt ggt cca gga agt gga aag ggt act	Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr	385		
115	120	125		
cag agt ttg aaa att gca gaa cga tat gga ttc caa tac att tct gtg	Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile Ser Val	433		
130	135	140		
gga gaa tta tta aga aag aag atc cac agt acc agc agc aat agg aaa	Gly Glu Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser Asn Arg Lys	481		
145	150	155	160	
tgg agt ctt att gcc aag ata att aca act gga gaa ttg gcc cca cag	Trp Ser Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu Ala Pro Gln	529		
165	170	175		
gaa aca aca att aca gag ata aaa caa aaa ttg atg caa ata cct gat	Glu Thr Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln Ile Pro Asp	577		
180	185	190		
gaa gag ggc att gtt att gat gga ttt cca aga gat gtt gcc cag gct	Glu Glu Gly Ile Val Ile Asp Gly Phe Pro Arg Asp Val Ala Gln Ala	625		
195	200	205		
cta tct ttt gag gac caa atc tgt acc ccc gat ttg gtg gta ttc ctg	Leu Ser Phe Glu Asp Gln Ile Cys Thr Pro Asp Leu Val Val Phe Leu	673		
210	215	220		
gct tgt gct aat cag aga ctc aaa gaa aga tta ctg aag cgt gca gaa	Ala Cys Ala Asn Gln Arg Leu Lys Glu Arg Leu Leu Lys Arg Ala Glu	721		
225	230	235	240	

cag cag ggc cga cca gac gac aat gta aaa gct acc caa agg aga cta	769
Gln Gln Gly Arg Pro Asp Asp Asn Val Lys Ala Thr Gln Arg Arg Leu	
245 250 255	
atg aac ttc aag cag aat gct gct cca ttg gtt aaa tac ttc cag gaa	817
Met Asn Phe Lys Gln Asn Ala Ala Pro Leu Val Lys Tyr Phe Gln Glu	
260 265 270	
aag ggg ctc atc atg aca ttt gat gcc gac cgc gat gag gat gag gtg	865
Lys Gly Leu Ile Met Thr Phe Asp Ala Asp Arg Asp Glu Asp Glu Val	
275 280 285	
ttc tat gac atc agc atg gca gtt gac aac aag tta ttt cca aac aaa	913
Phe Tyr Asp Ile Ser Met Ala Val Asp Asn Lys Leu Phe Pro Asn Lys	
290 295 300	
gag gct gca gca ggt tca agt gac ctt gat cct tcg atg ata ttg gac	961
Glu Ala Ala Ala Gly Ser Ser Asp Leu Asp Pro Ser Met Ile Leu Asp	
305 310 315 320	
act gga gag atc att gat aca gga tct gat tat gaa gat cag ggt gat	1009
Thr Gly Glu Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp Gln Gly Asp	
325 330 335	
gac cag tta aat gta ttt gga gag gac act atg gga ggt ttc atg gaa	1057
Asp Gln Leu Asn Val Phe Gly Glu Asp Thr Met Gly Gly Phe Met Glu	
340 345 350	
gat ttg aga aag tgt aaa att att ttc ata att ggt ggt cct ggc tct	1105
Asp Leu Arg Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly Pro Gly Ser	
355 360 365	
ggc aaa ggc aca cag tgt gaa aag ctg gtg gaa aaa tat gga ttt aca	1153
Gly Lys Gly Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr Gly Phe Thr	
370 375 380	
cat ctc tca act ggc gag ctc ctg cgt gag gaa ctg gca tca gaa tct	1201
His Leu Ser Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala Ser Glu Ser	
385 390 395 400	
gaa aga agc aaa ttg atc aga gac att atg gaa cgt gga gac ctg gtg	1249
Glu Arg Ser Lys Leu Ile Arg Asp Ile Met Glu Arg Gly Asp Leu Val	
405 410 415	
ccc tca ggc atc gtt ttg gag ctc ctg aag gag gcc atg gtg gcc agc	1297
Pro Ser Gly Ile Val Leu Glu Leu Leu Lys Glu Ala Met Val Ala Ser	
420 425 430	
ctc ggg gac acc agg ggc ttc ctg att gac ggc tat cct cgg gag gtg	1345
Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp Gly Tyr Pro Arg Glu Val	
435 440 445	
aag caa ggg gaa gag ttc gga cgc agg att gga gac cca cag ttg gtg	1393
Lys Gln Gly Glu Glu Phe Gly Arg Arg Ile Gly Asp Pro Gln Leu Val	
450 455 460	

atc tgt atg gac tgc tcg gca gac acc atg acc aac cgc ctt ctc caa 1441
 Ile Cys Met Asp Cys Ser Ala Asp Thr Met Thr Asn Arg Leu Leu Gln
 465 470 475 480

agg agc cgg agc agc ctg cct gtg gac gac acc acc aag acc atc gcc 1489
 Arg Ser Arg Ser Ser Leu Pro Val Asp Asp Thr Thr Lys Thr Ile Ala
 485 490 495

aag cgc cta gaa gcc tac tac cga gcg tcc atc ccc gtg atc gcc tac 1537
 Lys Arg Leu Glu Ala Tyr Tyr Arg Ala Ser Ile Pro Val Ile Ala Tyr
 500 505 510

tac gag aca aaa aca cag cta cac aag ata aat gca gag gga aca cca 1585
 Tyr Glu Thr Lys Thr Gln Leu His Lys Ile Asn Ala Glu Gly Thr Pro
 515 520 525

gag gac gtt ttt ctt caa ctc tgc aca gct att gac tct att att ttc 1633
 Glu Asp Val Phe Leu Gln Leu Cys Thr Ala Ile Asp Ser Ile Ile Phe
 530 535 540

gtc gac ggc 1642
 Val Asp Gly
 545

<210> 34
 <211> 547
 <212> PRT
 <213> Homo sapiens

<400> 34
 Thr Arg Ser Pro Thr Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala
 1 5 10 15
 Arg Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met
 20 25 30
 Cys Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln
 35 40 45
 Lys Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe
 50 55 60
 Val Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser
 65 70 75 80
 Arg Arg Ser Phe Leu Arg Asn Glu Ser Asp Thr Asp Leu Ser Glu Thr
 85 90 95
 Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr Arg Pro Arg
 100 105 110
 Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr
 115 120 125
 Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile Ser Val
 130 135 140

Gly	Glu	Leu	Leu	Arg	Lys	Lys	Ile	His	Ser	Thr	Ser	Ser	Asn	Arg	Lys	145	150	155	160
Trp	Ser	Leu	Ile	Ala	Lys	Ile	Ile	Thr	Thr	Gly	Glu	Leu	Ala	Pro	Gln	165	170	175	
Glu	Thr	Thr	Ile	Thr	Glu	Ile	Lys	Gln	Lys	Leu	Met	Gln	Ile	Pro	Asp	180	185	190	
Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val	Ala	Gln	Ala	195	200	205	
Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Leu	Val	Val	Phe	Leu	210	215	220	
Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys	Arg	Ala	Glu	225	230	235	240
Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln	Arg	Arg	Leu	245	250	255	
Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr	Phe	Gln	Glu	260	265	270	
Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp	Ala	Asp	Arg	Asp	Glu	Asp	Glu	Val	275	280	285	
Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val	Asp	Asn	Lys	Leu	Phe	Pro	Asn	Lys	290	295	300	
Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ser	Met	Ile	Leu	Asp	305	310	315	320
Thr	Gly	Glu	Ile	Ile	Asp	Thr	Gly	Ser	Asp	Tyr	Glu	Asp	Gln	Gly	Asp	325	330	335	
Asp	Gln	Leu	Asn	Val	Phe	Gly	Glu	Asp	Thr	Met	Gly	Gly	Phe	Met	Glu	340	345	350	
Asp	Leu	Arg	Lys	Cys	Lys	Ile	Ile	Phe	Ile	Ile	Gly	Gly	Pro	Gly	Ser	355	360	365	
Gly	Lys	Gly	Thr	Gln	Cys	Glu	Lys	Leu	Val	Glu	Lys	Tyr	Gly	Phe	Thr	370	375	380	
His	Leu	Ser	Thr	Gly	Glu	Leu	Leu	Arg	Glu	Glu	Leu	Ala	Ser	Glu	Ser	385	390	395	400
Glu	Arg	Ser	Lys	Leu	Ile	Arg	Asp	Ile	Met	Glu	Arg	Gly	Asp	Leu	Val	405	410	415	
Pro	Ser	Gly	Ile	Val	Leu	Glu	Leu	Leu	Lys	Glu	Ala	Met	Val	Ala	Ser	420	425	430	
Leu	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Ile	Asp	Gly	Tyr	Pro	Arg	Glu	Val	435	440	445	

Lys Gln Gly Glu Glu Phe Gly Arg Arg Ile Gly Asp Pro Gln Leu Val
 450 455 460
 Ile Cys Met Asp Cys Ser Ala Asp Thr Met Thr Asn Arg Leu Leu Gln
 465 470 475 480
 Arg Ser Arg Ser Ser Leu Pro Val Asp Asp Thr Thr Lys Thr Ile Ala
 485 490 495
 Lys Arg Leu Glu Ala Tyr Tyr Arg Ala Ser Ile Pro Val Ile Ala Tyr
 500 505 510
 Tyr Glu Thr Lys Thr Gln Leu His Lys Ile Asn Ala Glu Gly Thr Pro
 515 520 525
 Glu Asp Val Phe Leu Gln Leu Cys Thr Ala Ile Asp Ser Ile Ile Phe
 530 535 540
 Val Asp Gly
 545

<210> 35
 <211> 1842
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (375)..(1625)

<400> 35
 gcggccgcgc tgcctggcag cccgggaagc cgcggcacag ctgctcggcg cctgcagctc 60
 cggctcgggg gctggaaccg aagcgggggc ggcgggagcg cggagaccac agccccggg 120
 gagaggcgga gggggtcctt ggcctgggcg gagaggctga gctgagtgcg cgtgagaaag 180
 agggctgcac cgctgctcgg cgcggactct gccagcccca gcttcagccc cggctcaggt 240
 cgccgcagcc cgggagcctc cccgcttgcg cccaaggca cgcgcggcac agccatgaac 300
 accaacgatg ccaaggagta tctggcccgg agggaaatcc ctgagttata tttgagagcc 360
 ttttgaatgg actg atg tgt tct aag ccc gaa gat cca gta gaa tac ttg 410
 Met Cys Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu
 1 5 10
 gaa agt tgt tta caa aaa gta aag gaa ctg ggt ggc tgt gac aag gtg 458
 Glu Ser Cys Leu Gln Lys Val Lys Glu Leu Gly Gly Cys Asp Lys Val
 15 20 25
 aaa tgg gat aca ttt gta agc cag gaa aag aag acc tta cct cca cta 506
 Lys Trp Asp Thr Phe Val Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu
 30 35 40
 aat gga gga cag tca cgg aga tcc ttt cta aga aat gta atg cct gaa 554
 Asn Gly Gly Gln Ser Arg Arg Ser Phe Leu Arg Asn Val Met Pro Glu

45	50	55	60	
aac tca aac ttt cca tat cgg cgg tat gac cgg ctc cct cca atc cat				602
Asn Ser Asn Phe Pro Tyr Arg Arg Tyr Asp Arg Leu Pro Pro Ile His	65	70	75	
caa ttc tcc ata gaa agt gac acg gat ctc tct gag act gcg gag ttg				650
Gln Phe Ser Ile Glu Ser Asp Thr Asp Leu Ser Glu Thr Ala Glu Leu	80	85	90	
att gag gag tat gag gtt ttt gat cct acc aga cct cga cca aaa atc				698
Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr Arg Pro Arg Pro Lys Ile	95	100	105	
att ctt gtt ata ggt ggt cca gga agt gga aag ggt act cag agt ttg				746
Ile Leu Val Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Ser Leu	110	115	120	
aaa att gca gaa cga tat gga ttc caa tac att tct gtg gga gaa tta				794
Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile Ser Val Gly Glu Leu	125	130	135	140
tta aga aag aag atc cac agt acc agc agc aat agg aaa tgg agt ctt				842
Leu Arg Lys Lys Ile His Ser Thr Ser Ser Asn Arg Lys Trp Ser Leu	145	150	155	
att gcc aag ata att aca act gga gaa ttg gcc cca cag gaa aca aca				890
Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu Ala Pro Gln Glu Thr Thr	160	165	170	
att aca gag ata aaa caa aaa ttg atg caa ata cct gat gaa gag ggc				938
Ile Thr Glu Ile Lys Gln Lys Leu Met Gln Ile Pro Asp Glu Glu Gly	175	180	185	
att gtt att gat gga ttt cca aga gat gtt gcc cag gct cta tct ttt				986
Ile Val Ile Asp Gly Phe Pro Arg Asp Val Ala Gln Ala Leu Ser Phe	190	195	200	
gag gac cag atc tgt acc ccc gat ttg gtg gta ttc ctg gct tgt gct				1034
Glu Asp Gln Ile Cys Thr Pro Asp Leu Val Val Phe Leu Ala Cys Ala	205	210	215	220
aat cag aga ctc aaa gaa aga tta ctg aag cgt gca gaa cag cag ggc				1082
Asn Gln Arg Leu Lys Glu Arg Leu Leu Lys Arg Ala Glu Gln Gln Gly	225	230	235	
cga cca gac gac aat gta aaa gct acc caa agg aga cta atg aac ttc				1130
Arg Pro Asp Asp Asn Val Lys Ala Thr Gln Arg Arg Leu Met Asn Phe	240	245	250	
aag cag aat gct gct cca ttg gtt aaa tac ttc cag gaa aag ggg ctc				1178
Lys Gln Asn Ala Ala Pro Leu Val Lys Tyr Phe Gln Glu Lys Gly Leu	255	260	265	
atc atg aca ttt gat gcc gac cgc gat gag gat gag gtg ttc tat gac				1226
Ile Met Thr Phe Asp Ala Asp Arg Asp Glu Asp Glu Val Phe Tyr Asp	270	275	280	

atc agc atg gca gtt gac aac aag tta ttt cca aac aaa gag gct gca 1274
 Ile Ser Met Ala Val Asp Asn Lys Leu Phe Pro Asn Lys Glu Ala Ala
 285 290 295 300

gca ggt tca agt gac ctt gat cct tcg atg ata ttg gac act gga gag 1322
 Ala Gly Ser Ser Asp Leu Asp Pro Ser Met Ile Leu Asp Thr Gly Glu
 305 310 315

atc att gat aca gga tct gat tat gaa gat cag ggt gat gac cag tta 1370
 Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp Gln Gly Asp Asp Gln Leu
 320 325 330

aat gta ttt gga gag gac act atg gga ggt ttc atg gaa gat ttg aga 1418
 Asn Val Phe Gly Glu Asp Thr Met Gly Gly Phe Met Glu Asp Leu Arg
 335 340 345

aag tgt aaa att att ttc ata att ggt ggt cct ggc tct ggc aaa ggc 1466
 Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly
 350 355 360

aca cag tgt gaa aag ctg gtg gaa aaa tat gga ttt aca cat ctc tca 1514
 Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser
 365 370 375 380

act ggc gag ctc ctg cgt gag gaa ctg gca tca gaa tct gaa aga agc 1562
 Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser
 385 390 395

aaa ttg atc aga gac att atg gaa cgt gga gac ctg gtg ccc tca ggc 1610
 Lys Leu Ile Arg Asp Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly
 400 405 410

atc gtt tgg agc tcc tgaaggaggc atggtggcag ctcggggaca ccaggggctt 1665
 Ile Val Trp Ser Ser
 415

ctgatgacgg ttatctcggg aggggaagca ggggaagagt cggacggcag atggagacca 1725

acagtgggac tggatggact gcccgaaaca ccagacaacg cttccaaagg acggagattg 1785

ctgggagaac acaaaaaacag gaacgcaagc aaacgaagga accagggagc ccagaaa 1842

<210> 36
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Cys Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu
 1 5 10 15
 Gln Lys Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr
 20 25 30
 Phe Val Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln
 35 40 45

Ile Phe Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu
355 360 365

Lys Leu Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu Leu
370 375 380

Leu Arg Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg
385 390 395 400

Asp Ile Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Trp Ser
405 410 415

Ser

<210> 37
<211> 1714
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (17)..(1705)

<400> 37
caccagatct cccacc atg aac acc aac gat gcc aag gag tat ctg gcc cgg 52
Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg
1 5 10

agg gaa atc cct cag ctt ttt gag agc ctt ttg aat gga ctg atg tgt 100
Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys
15 20 25

tct aag ccc gaa gat cca gta gaa tac ttg gaa agt tgt tta caa aaa 148
Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys
30 35 40

gta aag gaa ctg ggt ggc tgt gac aag gtg aaa tgg gat aca ttt gta 196
Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val
45 50 55 60

agc cag gaa aag aag acc tta cct cca cta aat gga gga cag tca cgg 244
Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg
65 70 75

aga tcc ttt cta aga aat gta atg cct gaa aac tca aac ttt cca tat 292
Arg Ser Phe Leu Arg Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr
80 85 90

cgg cgg tat gac cgg ctc cct cca atc cat caa ttc tcc ata gaa agt 340
Arg Arg Tyr Asp Arg Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser
95 100 105

gac acg gat ctc tct gag act gca gag ttg att gag gag tat gag gtt 388
Asp Thr Asp Leu Ser Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val
110 115 120

ttt gat cct acc aga cct cga cca aaa atc att ctt gtt ata ggt ggt	436
Phe Asp Pro Thr Arg Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly	
125 130 135 140	
cca gga agt gga aag ggt act cag agt ttg aaa att gca gaa cga tat	484
Pro Gly Ser Gly Lys Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr	
145 150 155	
gga ttc caa tac att tct gtg gga gaa tta tta aga aag aag atc cac	532
Gly Phe Gln Tyr Ile Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His	
160 165 170	
agt acc agc agc aat agg aaa tgg agt ctt att gcc aag ata att aca	580
Ser Thr Ser Ser Asn Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr	
175 180 185	
act gga gaa ttg gcc cca cag gaa aca aca att aca gag ata aaa caa	628
Thr Gly Glu Leu Ala Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln	
190 195 200	
aaa ttg atg caa ata cct gat gaa gag ggc att gtt att gat gga ttt	676
Lys Leu Met Gln Ile Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe	
205 210 215 220	
cca aga gat gtt gcc cag gct cta tct ttt gag gac caa atc tgt acc	724
Pro Arg Asp Val Ala Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr	
225 230 235	
ccc gat ttg gtg gta ttc ctg gct tgt gct aat cag aga ctc aaa gaa	772
Pro Asp Leu Val Val Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys Glu	
240 245 250	
aga tta ctg aag cgt gca gaa cag cag ggc cga cca gac gac aat gta	820
Arg Leu Leu Lys Arg Ala Glu Gln Gln Gly Arg Pro Asp Asp Asn Val	
255 260 265	
aaa gct acc caa agg aga cta atg aac ttc aag cag aat gct gct cca	868
Lys Ala Thr Gln Arg Arg Leu Met Asn Phe Lys Gln Asn Ala Ala Pro	
270 275 280	
ttg gtt aaa tac ttc cag gaa aag ggg ctc atc atg aca ttt gat gcc	916
Leu Val Lys Tyr Phe Gln Glu Lys Gly Leu Ile Met Thr Phe Asp Ala	
285 290 295 300	
gac cgc gat gag gat gag gtg ttc tat gac atc agc atg gca gtt gac	964
Asp Arg Asp Glu Asp Glu Val Phe Tyr Asp Ile Ser Met Ala Val Asp	
305 310 315	
aac aag tta ttt cca aac aaa gag gct gca gca ggt tca agt gac ctt	1012
Asn Lys Leu Phe Pro Asn Lys Glu Ala Ala Ala Gly Ser Ser Asp Leu	
320 325 330	
gat cct tcg atg ata ttg gac act gga gag atc att gat aca gga tct	1060
Asp Pro Ser Met Ile Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly Ser	
335 340 345	

gat tat gaa gat cag ggt gat gac cag tta aat gta ttt gga gag gac	1108
Asp Tyr Glu Asp Gln Gly Asp Asp Gln Leu Asn Val Phe Gly Glu Asp	
350 355 360	
act atg gga ggt ttc atg gaa gat ttg aga aag tgt aaa att att ttc	1156
Thr Met Gly Gly Phe Met Glu Asp Leu Arg Lys Cys Lys Ile Ile Phe	
365 370 375 380	
ata att ggt ggt cct ggc tct ggc aaa ggc aca cag tgt gaa aag ctg	1204
Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu	
385 390 395	
gtg gaa aaa tat gga ttt aca cat ctc tca act ggc gag ctc ctg cgt	1252
Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg	
400 405 410	
gag gaa ctg gca tca gaa tct gaa aga agc aaa ttg atc aga gac att	1300
Glu Glu Leu Ala Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp Ile	
415 420 425	
atg gaa cgt gga gac ctg gtg ccc tca ggc atc gtt ttg gag ctc ctg	1348
Met Glu Arg Gly Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu Leu	
430 435 440	
aag gag gcc atg gtg gcc agc ctc ggg gac acc agg ggc ttc ctg att	1396
Lys Glu Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile	
445 450 455 460	
gac ggc tat cct cgg gag gtg aag caa ggg gaa gag ttc gga cgc agg	1444
Asp Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe Gly Arg Arg	
465 470 475	
att gga gac cca cag ttg gtg atc tgt atg gac tgc tcg gca gac acc	1492
Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser Ala Asp Thr	
480 485 490	
atg acc aac cgc ctt ctc caa agg agc cgg agc agc ctg cct gtg gac	1540
Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu Pro Val Asp	
495 500 505	
gac acc acc aag acc atc gcc aag cgc cta gaa gcc tac tac cga gcg	1588
Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg Ala	
510 515 520	
tcc atc ccc gtg atc gcc tac tac gag aca aaa aca cag cta cac aag	1636
Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His Lys	
525 530 535 540	
ata aat gca gag gga aca cca gag gac gtt ttt ctt caa ctc tgc aca	1684
Ile Asn Ala Glu Gly Thr Pro Glu Asp Val Phe Leu Gln Leu Cys Thr	
545 550 555	
gct att gac tct att att ttc gtcgacggc	1714
Ala Ile Asp Ser Ile Ile Phe	
560	

<210> 38

<211> 563
 <212> PRT
 <213> Homo sapiens

<400> 38

Met	Asn	Thr	Asn	Asp	Ala	Lys	Glu	Tyr	Leu	Ala	Arg	Arg	Glu	Ile	Pro
1				5					10					15	
Gln	Leu	Phe	Glu	Ser	Leu	Leu	Asn	Gly	Leu	Met	Cys	Ser	Lys	Pro	Glu
			20					25					30		
Asp	Pro	Val	Glu	Tyr	Leu	Glu	Ser	Cys	Leu	Gln	Lys	Val	Lys	Glu	Leu
		35					40					45			
Gly	Gly	Cys	Asp	Lys	Val	Lys	Trp	Asp	Thr	Phe	Val	Ser	Gln	Glu	Lys
	50					55					60				
Lys	Thr	Leu	Pro	Pro	Leu	Asn	Gly	Gly	Gln	Ser	Arg	Arg	Ser	Phe	Leu
65					70					75					80
Arg	Asn	Val	Met	Pro	Glu	Asn	Ser	Asn	Phe	Pro	Tyr	Arg	Arg	Tyr	Asp
				85					90					95	
Arg	Leu	Pro	Pro	Ile	His	Gln	Phe	Ser	Ile	Glu	Ser	Asp	Thr	Asp	Leu
			100					105					110		
Ser	Glu	Thr	Ala	Glu	Leu	Ile	Glu	Glu	Tyr	Glu	Val	Phe	Asp	Pro	Thr
		115					120					125			
Arg	Pro	Arg	Pro	Lys	Ile	Ile	Leu	Val	Ile	Gly	Gly	Pro	Gly	Ser	Gly
	130					135					140				
Lys	Gly	Thr	Gln	Ser	Leu	Lys	Ile	Ala	Glu	Arg	Tyr	Gly	Phe	Gln	Tyr
145					150					155					160
Ile	Ser	Val	Gly	Glu	Leu	Leu	Arg	Lys	Lys	Ile	His	Ser	Thr	Ser	Ser
				165					170					175	
Asn	Arg	Lys	Trp	Ser	Leu	Ile	Ala	Lys	Ile	Ile	Thr	Thr	Gly	Glu	Leu
			180					185					190		
Ala	Pro	Gln	Glu	Thr	Thr	Ile	Thr	Glu	Ile	Lys	Gln	Lys	Leu	Met	Gln
		195					200					205			
Ile	Pro	Asp	Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val
	210					215					220				
Ala	Gln	Ala	Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Leu	Val
225					230					235					240
Val	Phe	Leu	Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys
				245					250					255	
Arg	Ala	Glu	Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln
		260						265					270		
Arg	Arg	Leu	Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr

275					280					285						
Phe	Gln	Glu	Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp	Ala	Asp	Arg	Asp	Glu	
290					295					300						
Asp	Glu	Val	Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val	Asp	Asn	Lys	Leu	Phe	
305					310					315					320	
Pro	Asn	Lys	Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ser	Met	
325					330					335						
Ile	Leu	Asp	Thr	Gly	Glu	Ile	Ile	Asp	Thr	Gly	Ser	Asp	Tyr	Glu	Asp	
340					345					350						
Gln	Gly	Asp	Asp	Gln	Leu	Asn	Val	Phe	Gly	Glu	Asp	Thr	Met	Gly	Gly	
355					360					365						
Phe	Met	Glu	Asp	Leu	Arg	Lys	Cys	Lys	Ile	Ile	Phe	Ile	Ile	Gly	Gly	
370					375					380						
Pro	Gly	Ser	Gly	Lys	Gly	Thr	Gln	Cys	Glu	Lys	Leu	Val	Glu	Lys	Tyr	
385					390					395					400	
Gly	Phe	Thr	His	Leu	Ser	Thr	Gly	Glu	Leu	Leu	Arg	Glu	Glu	Leu	Ala	
405					410					415						
Ser	Glu	Ser	Glu	Arg	Ser	Lys	Leu	Ile	Arg	Asp	Ile	Met	Glu	Arg	Gly	
420					425					430						
Asp	Leu	Val	Pro	Ser	Gly	Ile	Val	Leu	Glu	Leu	Leu	Lys	Glu	Ala	Met	
435					440					445						
Val	Ala	Ser	Leu	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Ile	Asp	Gly	Tyr	Pro	
450					455					460						
Arg	Glu	Val	Lys	Gln	Gly	Glu	Glu	Phe	Gly	Arg	Arg	Ile	Gly	Asp	Pro	
465					470					475					480	
Gln	Leu	Val	Ile	Cys	Met	Asp	Cys	Ser	Ala	Asp	Thr	Met	Thr	Asn	Arg	
485					490					495						
Leu	Leu	Gln	Arg	Ser	Arg	Ser	Ser	Leu	Pro	Val	Asp	Asp	Thr	Thr	Lys	
500					505					510						
Thr	Ile	Ala	Lys	Arg	Leu	Glu	Ala	Tyr	Tyr	Arg	Ala	Ser	Ile	Pro	Val	
515					520					525						
Ile	Ala	Tyr	Tyr	Glu	Thr	Lys	Thr	Gln	Leu	His	Lys	Ile	Asn	Ala	Glu	
530					535					540						
Gly	Thr	Pro	Glu	Asp	Val	Phe	Leu	Gln	Leu	Cys	Thr	Ala	Ile	Asp	Ser	
545					550					555					560	
Ile Ile Phe																

<210> 39

<211> 1714
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)..(1702)

<400> 39
 caccggatcc acc atg aac acc aac gat gcc aag gag tat ctg gcc cgg 49
 Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg
 1 5 10

agg gaa atc cct cag ctt ttt gag agc ctt ttg aat gga ctg atg tgt 97
 Arg Glu Ile Pro Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys
 15 20 25

tct aag ccc gaa gat cca gta gaa tac ttg gaa agt tgt tta caa aaa 145
 Ser Lys Pro Glu Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys
 30 35 40

gta aag gaa ctg ggt ggc tgt gac aag gtg aaa tgg gat aca ttt gta 193
 Val Lys Glu Leu Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val
 45 50 55 60

agc cag gaa aag aag acc tta cct cca cta aat gga gga cag tca cgg 241
 Ser Gln Glu Lys Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg
 65 70 75

aga tcc ttt cta aga aat gta atg cct gaa aac tca aac ttt cca tat 289
 Arg Ser Phe Leu Arg Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr
 80 85 90

cgg cgg tat gac cgg ctc cct cca atc cat caa ttc tcc ata gaa agt 337
 Arg Arg Tyr Asp Arg Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser
 95 100 105

gac acg gat ctc tct gag act gca gag ttg att gag gag tat gag gtt 385
 Asp Thr Asp Leu Ser Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val
 110 115 120

ttt gat cct acc aga cct cga cca aaa atc att ctt gtt ata ggt ggt 433
 Phe Asp Pro Thr Arg Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly
 125 130 135 140

cca gga agt gga aag ggt act cag agt ttg aaa att gca gaa cga tat 481
 Pro Gly Ser Gly Lys Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr
 145 150 155

gga ttc caa tac att tct gtg gga gaa tta tta aga aag aag atc cac 529
 Gly Phe Gln Tyr Ile Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His
 160 165 170

agt acc agc agc aat agg aaa tgg agt ctt att gcc aag ata att aca 577
 Ser Thr Ser Ser Asn Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr
 175 180 185

act gga gaa ttg gcc cca cag gaa aca aca att aca gag ata aaa caa	625
Thr Gly Glu Leu Ala Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln	
190 195 200	
aaa ttg atg caa ata cct gat gaa gag ggc att gtt att gat gga ttt	673
Lys Leu Met Gln Ile Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe	
205 210 215 220	
cca aga gat gtt gcc cag gct cta tct ttt gag gac caa atc tgt acc	721
Pro Arg Asp Val Ala Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr	
225 230 235	
ccc gat ttg gtg gta ttc ctg gct tgt gct aat cag aga ctc aaa gaa	769
Pro Asp Leu Val Val Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys Glu	
240 245 250	
aga tta ctg aag cgt gca gaa cag cag ggc cga cca gac gac aat gta	817
Arg Leu Leu Lys Arg Ala Glu Gln Gln Gly Arg Pro Asp Asp Asn Val	
255 260 265	
aaa gct acc caa agg aga cta atg aac ttc aag cag aat gct gct cca	865
Lys Ala Thr Gln Arg Arg Leu Met Asn Phe Lys Gln Asn Ala Ala Pro	
270 275 280	
ttg gtt aaa tac ttc cag gaa aag ggg ctc atc atg aca ttt gat gcc	913
Leu Val Lys Tyr Phe Gln Glu Lys Gly Leu Ile Met Thr Phe Asp Ala	
285 290 295 300	
gac cgc gat gag gat gag gtg ttc tat gac atc agc atg gca gtt gac	961
Asp Arg Asp Glu Asp Glu Val Phe Tyr Asp Ile Ser Met Ala Val Asp	
305 310 315	
aac aag tta ttt cca aac aaa gag gct gca gca ggt tca agt gac ctt	1009
Asn Lys Leu Phe Pro Asn Lys Glu Ala Ala Ala Gly Ser Ser Asp Leu	
320 325 330	
gat cct tcg atg ata ttg gac act gga gag atc att gat aca gga tct	1057
Asp Pro Ser Met Ile Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly Ser	
335 340 345	
gat tat gaa gat cag ggt gat gac cag tta aat gta ttt gga gag gac	1105
Asp Tyr Glu Asp Gln Gly Asp Asp Gln Leu Asn Val Phe Gly Glu Asp	
350 355 360	
act atg gga ggt ttc atg gaa gat ttg aga aag tgt aaa att att ttc	1153
Thr Met Gly Gly Phe Met Glu Asp Leu Arg Lys Cys Lys Ile Ile Phe	
365 370 375 380	
ata att ggt ggt cct ggc tct ggc aaa ggc aca cag tgt gaa aag ctg	1201
Ile Ile Gly Gly Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu	
385 390 395	
gtg gaa aaa tat gga ttt aca cat ctc tca act ggc gag ctc ctg cgt	1249
Val Glu Lys Tyr Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg	
400 405 410	
gag gaa ctg gca tca gaa tct gaa aga agc aaa ttg atc aga gac att	1297

Glu	Glu	Leu	Ala	Ser	Glu	Ser	Glu	Arg	Ser	Lys	Leu	Ile	Arg	Asp	Ile		
		415					420					425					
atg	gaa	cgt	gga	gac	ctg	gtg	ccc	tca	ggc	atc	gtt	ttg	gag	ctc	ctg	1345	
Met	Glu	Arg	Gly	Asp	Leu	Val	Pro	Ser	Gly	Ile	Val	Leu	Glu	Leu	Leu		
	430					435					440						
aag	gag	gcc	atg	gtg	gcc	agc	ctc	ggg	gac	acc	agg	ggc	ttc	ctg	att	1393	
Lys	Glu	Ala	Met	Val	Ala	Ser	Leu	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Ile		
445					450					455					460		
gac	ggc	tat	cct	cgg	gag	gtg	aag	caa	ggg	gaa	gag	ttc	gga	cgc	agg	1441	
Asp	Gly	Tyr	Pro	Arg	Glu	Val	Lys	Gln	Gly	Glu	Glu	Phe	Gly	Arg	Arg		
				465					470					475			
att	gga	gac	cca	cag	ttg	gtg	atc	tgt	atg	gac	tgc	tcg	gca	gac	acc	1489	
Ile	Gly	Asp	Pro	Gln	Leu	Val	Ile	Cys	Met	Asp	Cys	Ser	Ala	Asp	Thr		
			480					485					490				
atg	acc	aac	cgc	ctt	ctc	caa	agg	agc	cgg	agc	agc	ctg	cct	gtg	gac	1537	
Met	Thr	Asn	Arg	Leu	Leu	Gln	Arg	Ser	Arg	Ser	Ser	Leu	Pro	Val	Asp		
		495					500					505					
gac	acc	acc	aag	acc	atc	gcc	aag	cgc	cta	gaa	gcc	tac	tac	cga	gcg	1585	
Asp	Thr	Thr	Lys	Thr	Ile	Ala	Lys	Arg	Leu	Glu	Ala	Tyr	Tyr	Arg	Ala		
	510					515					520						
tcc	atc	ccc	gtg	atc	gcc	tac	tac	gag	aca	aaa	aca	cag	cta	cac	aag	1633	
Ser	Ile	Pro	Val	Ile	Ala	Tyr	Tyr	Glu	Thr	Lys	Thr	Gln	Leu	His	Lys		
525					530					535					540		
ata	aat	gca	gag	gga	aca	cca	gag	gac	gtt	ttt	ctt	caa	ctc	tgc	aca	1681	
Ile	Asn	Ala	Glu	Gly	Thr	Pro	Glu	Asp	Val	Phe	Leu	Gln	Leu	Cys	Thr		
				545					550					555			
gct	att	gac	tct	att	att	ttc	tagctcgagg	gc								1714	
Ala	Ile	Asp	Ser	Ile	Ile	Phe											
				560													

<210> 40
 <211> 563
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg Arg Glu Ile Pro
 1 5 10 15
 Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys Ser Lys Pro Glu
 20 25 30
 Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys Val Lys Glu Leu
 35 40 45
 Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val Ser Gln Glu Lys
 50 55 60

Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg Arg Ser Phe Leu
 65 70 75 80
 Arg Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr Arg Arg Tyr Asp
 85 90 95
 Arg Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser Asp Thr Asp Leu
 100 105 110
 Ser Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr
 115 120 125
 Arg Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly
 130 135 140
 Lys Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr
 145 150 155 160
 Ile Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser
 165 170 175
 Asn Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu
 180 185 190
 Ala Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln
 195 200 205
 Ile Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe Pro Arg Asp Val
 210 215 220
 Ala Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr Pro Asp Leu Val
 225 230 235 240
 Val Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys Glu Arg Leu Leu Lys
 245 250 255
 Arg Ala Glu Gln Gln Gly Arg Pro Asp Asp Asn Val Lys Ala Thr Gln
 260 265 270
 Arg Arg Leu Met Asn Phe Lys Gln Asn Ala Ala Pro Leu Val Lys Tyr
 275 280 285
 Phe Gln Glu Lys Gly Leu Ile Met Thr Phe Asp Ala Asp Arg Asp Glu
 290 295 300
 Asp Glu Val Phe Tyr Asp Ile Ser Met Ala Val Asp Asn Lys Leu Phe
 305 310 315 320
 Pro Asn Lys Glu Ala Ala Ala Gly Ser Ser Asp Leu Asp Pro Ser Met
 325 330 335
 Ile Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp
 340 345 350
 Gln Gly Asp Asp Gln Leu Asn Val Phe Gly Glu Asp Thr Met Gly Gly
 355 360 365

Phe Met Glu Asp Leu Arg Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly
 370 375 380
 Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr
 385 390 395 400
 Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala
 405 410 415
 Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp Ile Met Glu Arg Gly
 420 425 430
 Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu Leu Lys Glu Ala Met
 435 440 445
 Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp Gly Tyr Pro
 450 455 460
 Arg Glu Val Lys Gln Gly Glu Glu Phe Gly Arg Arg Ile Gly Asp Pro
 465 470 475 480
 Gln Leu Val Ile Cys Met Asp Cys Ser Ala Asp Thr Met Thr Asn Arg
 485 490 495
 Leu Leu Gln Arg Ser Arg Ser Ser Leu Pro Val Asp Asp Thr Thr Lys
 500 505 510
 Thr Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg Ala Ser Ile Pro Val
 515 520 525
 Ile Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His Lys Ile Asn Ala Glu
 530 535 540
 Gly Thr Pro Glu Asp Val Phe Leu Gln Leu Cys Thr Ala Ile Asp Ser
 545 550 555 560
 Ile Ile Phe

<210> 41
 <211> 3309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (295)..(1983)

<400> 41
 gcggcgcgc tgctggcag cccgggaagc cgcgccacag ctgctcggcg cctgcagctc 60
 cggctcgggg gctggaaccg aagcgggggc ggcgggagcg cggagaccac agccccggg 120
 gagaggcgga gggggtcctt ggcctgggcg gagaggctga gctgagtgcg cgtgagaaag 180
 agggctgcac cgctgctcgg cgcggaactct gccagcccca gcttcagccc cggctcaggt 240

cgccgcagcc	cgggagcctc	cccgccttgcg	cccccaaggca	cgcgcgggcac	agcc	atg	297
						Met	
						1	
aac acc aac gat gcc aag gag tat ctg gcc cgg agg gaa atc cct cag	345						
Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg Arg Glu Ile Pro Gln		5	10	15			
ctt ttt gag agc ctt ttg aat gga ctg atg tgt tct aag ccc gaa gat	393						
Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys Ser Lys Pro Glu Asp		20	25	30			
cca gta gaa tac ttg gaa agt tgt tta caa aaa gta aag gaa ctg ggt	441						
Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys Val Lys Glu Leu Gly		35	40	45			
ggc tgt gac aag gtg aaa tgg gat aca ttt gta agc cag gaa aag aag	489						
Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val Ser Gln Glu Lys Lys		50	55	60	65		
acc tta cct cca cta aat gga gga cag tca cgg aga tcc ttt cta aga	537						
Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg Arg Ser Phe Leu Arg		70	75	80			
aat gta atg cct gaa aac tca aac ttt cca tat cgg cgg tat gac cgg	585						
Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr Arg Arg Tyr Asp Arg		85	90	95			
ctc cct cca atc cat caa ttc tcc ata gaa agt gac acg gat ctc tct	633						
Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser Asp Thr Asp Leu Ser		100	105	110			
gag act gcg gag ttg att gag gag tat gag gtt ttt gat cct acc aga	681						
Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr Arg		115	120	125			
cct cga cca aaa atc att ctt gtt ata ggt ggt cca gga agt gga aag	729						
Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly Lys		130	135	140	145		
ggt act cag agt ttg aaa att gca gaa cga tat gga ttc caa tac att	777						
Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr Ile		150	155	160			
tct gtg gga gaa tta tta aga aag aag atc cac agt acc agc agc aat	825						
Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser Asn		165	170	175			
agg aaa tgg agt ctt att gcc aag ata att aca act gga gaa ttg gcc	873						
Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu Ala		180	185	190			
cca cag gaa aca aca att aca gag ata aaa caa aaa ttg atg caa ata	921						
Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln Ile		195	200	205			
cct gat gaa gag ggc att gtt att gat gga ttt cca aga gat gtt gcc	969						

Pro	Asp	Glu	Glu	Gly	Ile	Val	Ile	Asp	Gly	Phe	Pro	Arg	Asp	Val	Ala		
210					215					220					225		
cag	gct	cta	tct	ttt	gag	gac	caa	atc	tgt	acc	ccc	gat	ttt	gtg	gta		1017
Gln	Ala	Leu	Ser	Phe	Glu	Asp	Gln	Ile	Cys	Thr	Pro	Asp	Phe	Val	Val		
				230					235					240			
ttc	ctg	gct	tgt	gct	aat	cag	aga	ctc	aaa	gaa	aga	tta	ctg	aag	cgt		1065
Phe	Leu	Ala	Cys	Ala	Asn	Gln	Arg	Leu	Lys	Glu	Arg	Leu	Leu	Lys	Arg		
			245					250					255				
gca	gaa	cag	cag	ggc	cga	cca	gac	gac	aat	gta	aaa	gct	acc	caa	agg		1113
Ala	Glu	Gln	Gln	Gly	Arg	Pro	Asp	Asp	Asn	Val	Lys	Ala	Thr	Gln	Arg		
		260					265					270					
aga	cta	atg	aac	ttc	aag	cag	aat	gct	gct	cca	ttg	ggt	aaa	tac	ttc		1161
Arg	Leu	Met	Asn	Phe	Lys	Gln	Asn	Ala	Ala	Pro	Leu	Val	Lys	Tyr	Phe		
	275					280				285							
cag	gaa	aag	ggg	ctc	atc	atg	aca	ttt	gat	gcc	gac	cgc	gat	gag	gat		1209
Gln	Glu	Lys	Gly	Leu	Ile	Met	Thr	Phe	Asp	Ala	Asp	Arg	Asp	Glu	Asp		
290					295				300					305			
gag	gtg	ttc	tat	gac	atc	agc	atg	gca	gtt	gac	aac	aag	tta	ttt	cca		1257
Glu	Val	Phe	Tyr	Asp	Ile	Ser	Met	Ala	Val	Asp	Asn	Lys	Leu	Phe	Pro		
				310					315					320			
aac	aaa	gag	gct	gca	gca	ggg	tca	agt	gac	ctt	gat	cct	tcg	atg	ata		1305
Asn	Lys	Glu	Ala	Ala	Ala	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ser	Met	Ile		
		325					330					335					
ttg	gac	act	gga	gag	atc	att	gat	aca	gga	tct	gat	tat	gaa	gat	cag		1353
Leu	Asp	Thr	Gly	Glu	Ile	Ile	Asp	Thr	Gly	Ser	Asp	Tyr	Glu	Asp	Gln		
		340					345					350					
ggg	gat	gac	cag	tta	aat	gta	ttt	gga	gag	gac	act	atg	gga	ggg	ttc		1401
Gly	Asp	Asp	Gln	Leu	Asn	Val	Phe	Gly	Glu	Asp	Thr	Met	Gly	Gly	Phe		
	355					360					365						
atg	gaa	gat	ttg	aga	aag	tgt	aaa	att	att	ttc	ata	att	ggg	ggg	cct		1449
Met	Glu	Asp	Leu	Arg	Lys	Cys	Lys	Ile	Ile	Phe	Ile	Ile	Gly	Gly	Pro		
370					375					380				385			
ggc	tct	ggc	aaa	ggc	aca	cag	tgt	gaa	aag	ctg	gtg	gaa	aaa	tat	gga		1497
Gly	Ser	Gly	Lys	Gly	Thr	Gln	Cys	Glu	Lys	Leu	Val	Glu	Lys	Tyr	Gly		
				390					395					400			
ttt	aca	cat	ctc	tca	act	ggc	gag	ctc	ctg	cgt	gag	gaa	ctg	gca	tca		1545
Phe	Thr	His	Leu	Ser	Thr	Gly	Glu	Leu	Leu	Arg	Glu	Glu	Leu	Ala	Ser		
			405					410					415				
gaa	tct	gaa	aga	agc	aaa	ttg	atc	aga	gac	att	atg	gaa	cgt	gga	gac		1593,
Glu	Ser	Glu	Arg	Ser	Lys	Leu	Ile	Arg	Asp	Ile	Met	Glu	Arg	Gly	Asp		
		420					425					430					
ctg	gtg	ccc	tca	ggc	atc	gtt	ttg	gag	ctc	ctg	aag	gag	gcc	atg	gtg		1641
Leu	Val	Pro	Ser	Gly	Ile	Val	Leu	Glu	Leu	Leu	Lys	Glu	Ala	Met	Val		

435	440	445	
gcc agc ctc ggg gac acc agg ggc ttc ctg att gac ggc tat cct cgg			1689
Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp Gly Tyr Pro Arg			
450	455	460	465
gag gtg aag caa ggg gaa gag ttc gga cgc agg att gga gac cca cag			1737
Glu Val Lys Gln Gly Glu Glu Phe Gly Arg Arg Ile Gly Asp Pro Gln			
	470	475	480
ttg gtg atc tgt atg gac tgc tgc gca gac acc atg acc aac cgc ctt			1785
Leu Val Ile Cys Met Asp Cys Ser Ala Asp Thr Met Thr Asn Arg Leu			
	485	490	495
ctc caa agg agc cgg agc agc ctg cct gtg gac gac acc acc aag acc			1833
Leu Gln Arg Ser Arg Ser Ser Leu Pro Val Asp Asp Thr Thr Lys Thr			
	500	505	510
atc gcc aag cgc cta gaa gcc tac tac cga gcg tcc atc ccc gtg atc			1881
Ile Ala Lys Arg Leu Glu Ala Tyr Tyr Arg Ala Ser Ile Pro Val Ile			
	515	520	525
gcc tac tac gag aca aaa aca cag cta cac aag ata aat gca gag gga			1929
Ala Tyr Tyr Glu Thr Lys Thr Gln Leu His Lys Ile Asn Ala Glu Gly			
530	535	540	545
aca cca gag gac gtt ttt ctt caa ctc tgc aca gct att gac tct att			1977
Thr Pro Glu Asp Val Phe Leu Gln Leu Cys Thr Ala Ile Asp Ser Ile			
	550	555	560
att ttc tgaaggcaaa aatgcatggt tgtagaatg gaaacagaaa aacattaaaa			2033
Ile Phe			
agttcattcc ttaacacaat gtttcaagtt aaaccttttg tgtcaccgcc cccaccaaac			2093
caccacctcc taaatcctga cagcactggt tgcttcccag ctagacctgt gtgagaggtg			2153
tctggaaatc atgcatggtg tatttgggac tatatcaacc tattctccac acttcagaca			2213
actgtctgca ctcacggcac gcacactttg tatcatgcag gccacactca gagctagtca			2273
gtacatgaac agtgggtgcg tgccagtctg tgtccgttgt gatcacaggc cttgctagac			2333
cctgatcatc tggttctcct ctcatgaagc atccctaacc ccagtcaca ccttctctt			2393
acatactggt cccaatgga ggcccctggc ataggggaca gccctgggca tcttctttg			2453
gtgtctggct gttttgtcaa ctctcatcca ctgggtggctc agagccataa ggtgggttga			2513
ttacacaatg cttgtacat gatatagagg catcaagcaa gtaaaatttg acagaaattt			2573
taaaatatga agatgtatag ctttcccaag atgatggtaa aaccaggtt agtcatcagt			2633
aaccttctct attattatta ttttttagaa acttgggaata ctgtcattat ggctaagaga			2693
acaaatctga taaattgtgt aacctagtct cttctctaca tgggtgatgca tttcagcaat			2753

tataaattaa tataaatgac caaaagtaac ttaaaagcat gagatatttg ctatttcatt 2813
cattgggcac atatcaaatt ataattttga ttttaaattg tcacccatgt atttggtgcc 2873
aagcaagtaa aaaaataccc taacaaacct gatgtgggtg ggaggggcat gtcagtaagt 2933
ggtgtgttca atgtgtttgt ttcatatggg ccctttccag gagtttgcaa acctgtcat 2993
acccatatgc aaaactgtgt ttccttgcac taaaccagtg aagtttgggt tctcttttgt 3053
gctatcaatc agttgtaaaa tcagagcttc ttatatattc tactggaata actgcattctt 3113
ccactcagtc actacaaaaa agcatagttt cagtttgcac gaattttttt ttttttcttc 3173
aatggttgtg cagataagga tccatttctg ggatagaatt gtatttttta agtcattttt 3233
ttttcttgaa atggatatgt acaaataaaa ttaaattggaa gacaggaaaa aaaaaaaaaa 3293
aaaaaaaaa aaaaaa 3309

<210> 42
<211> 563
<212> PRT
<213> Homo sapiens

<400> 42
Met Asn Thr Asn Asp Ala Lys Glu Tyr Leu Ala Arg Arg Glu Ile Pro
1 5 10 15
Gln Leu Phe Glu Ser Leu Leu Asn Gly Leu Met Cys Ser Lys Pro Glu
20 25 30
Asp Pro Val Glu Tyr Leu Glu Ser Cys Leu Gln Lys Val Lys Glu Leu
35 40 45
Gly Gly Cys Asp Lys Val Lys Trp Asp Thr Phe Val Ser Gln Glu Lys
50 55 60
Lys Thr Leu Pro Pro Leu Asn Gly Gly Gln Ser Arg Arg Ser Phe Leu
65 70 75 80
Arg Asn Val Met Pro Glu Asn Ser Asn Phe Pro Tyr Arg Arg Tyr Asp
85 90 95
Arg Leu Pro Pro Ile His Gln Phe Ser Ile Glu Ser Asp Thr Asp Leu
100 105 110
Ser Glu Thr Ala Glu Leu Ile Glu Glu Tyr Glu Val Phe Asp Pro Thr
115 120 125
Arg Pro Arg Pro Lys Ile Ile Leu Val Ile Gly Gly Pro Gly Ser Gly
130 135 140
Lys Gly Thr Gln Ser Leu Lys Ile Ala Glu Arg Tyr Gly Phe Gln Tyr
145 150 155 160

Ile Ser Val Gly Glu Leu Leu Arg Lys Lys Ile His Ser Thr Ser Ser
 165 170 175
 Asn Arg Lys Trp Ser Leu Ile Ala Lys Ile Ile Thr Thr Gly Glu Leu
 180 185 190
 Ala Pro Gln Glu Thr Thr Ile Thr Glu Ile Lys Gln Lys Leu Met Gln
 195 200 205
 Ile Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe Pro Arg Asp Val
 210 215 220
 Ala Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr Pro Asp Phe Val
 225 230 235 240
 Val Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys Glu Arg Leu Leu Lys
 245 250 255
 Arg Ala Glu Gln Gln Gly Arg Pro Asp Asp Asn Val Lys Ala Thr Gln
 260 265 270
 Arg Arg Leu Met Asn Phe Lys Gln Asn Ala Ala Pro Leu Val Lys Tyr
 275 280 285
 Phe Gln Glu Lys Gly Leu Ile Met Thr Phe Asp Ala Asp Arg Asp Glu
 290 295 300
 Asp Glu Val Phe Tyr Asp Ile Ser Met Ala Val Asp Asn Lys Leu Phe
 305 310 315 320
 Pro Asn Lys Glu Ala Ala Ala Gly Ser Ser Asp Leu Asp Pro Ser Met
 325 330 335
 Ile Leu Asp Thr Gly Glu Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp
 340 345 350
 Gln Gly Asp Asp Gln Leu Asn Val Phe Gly Glu Asp Thr Met Gly Gly
 355 360 365
 Phe Met Glu Asp Leu Arg Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly
 370 375 380
 Pro Gly Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr
 385 390 395 400
 Gly Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala
 405 410 415
 Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp Ile Met Glu Arg Gly
 420 425 430
 Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu Leu Lys Glu Ala Met
 435 440 445
 Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp Gly Tyr Pro
 450 455 460

Arg	Glu	Val	Lys	Gln	Gly	Glu	Glu	Phe	Gly	Arg	Arg	Ile	Gly	Asp	Pro
465					470					475					480
Gln	Leu	Val	Ile	Cys	Met	Asp	Cys	Ser	Ala	Asp	Thr	Met	Thr	Asn	Arg
				485					490					495	
Leu	Leu	Gln	Arg	Ser	Arg	Ser	Ser	Leu	Pro	Val	Asp	Asp	Thr	Thr	Lys
			500					505					510		
Thr	Ile	Ala	Lys	Arg	Leu	Glu	Ala	Tyr	Tyr	Arg	Ala	Ser	Ile	Pro	Val
		515					520					525			
Ile	Ala	Tyr	Tyr	Glu	Thr	Lys	Thr	Gln	Leu	His	Lys	Ile	Asn	Ala	Glu
	530					535					540				
Gly	Thr	Pro	Glu	Asp	Val	Phe	Leu	Gln	Leu	Cys	Thr	Ala	Ile	Asp	Ser
545					550					555					560
Ile	Ile	Phe													

<210> 43
 <211> 3205
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(1145)

gacaagagct cagacctgag gagagtgact agcttctctg tgtcccaggt ggccaccttc																60
cactgtggaa	gctc	atg	gac	tcc	att	ggg	tct	tca	ggg	ttg	cgg	cag	ggg			110
		Met	Asp	Ser	Ile	Gly	Ser	Ser	Gly	Leu	Arg	Gln	Gly			
		1				5					10					
gaa gaa acc ctg agt tgc tct gag gag ggc ttg ccc ggg ccc tca gac																158
Glu Glu Thr Leu Ser Cys Ser Glu Glu Gly Leu Pro Gly Pro Ser Asp																
	15					20				25						
agc tca gag ctg gtg cag gag tgc ctg cag cag ttc aag gtg aca agg																206
Ser Ser Glu Leu Val Gln Glu Cys Leu Gln Gln Phe Lys Val Thr Arg																
	30				35				40							
gca cag cta cag cag atc caa gcc agc ctc ttg ggt tcc atg gag cag																254
Ala Gln Leu Gln Gln Ile Gln Ala Ser Leu Leu Gly Ser Met Glu Gln																
	45				50			55						60		
gcg ctg agg gga cag gcc agc cct gcc cct gcg gtc cgg atg ctg cct																302
Ala Leu Arg Gly Gln Ala Ser Pro Ala Pro Ala Val Arg Met Leu Pro																
			65				70						75			
aca tac gtg ggg tcc acc cca cat ggc act gag caa gga gac ttc gtg																350
Thr Tyr Val Gly Ser Thr Pro His Gly Thr Glu Gln Gly Asp Phe Val																
	80						85						90			

gtg	ctg	gag	ctg	ggg	gcc	aca	ggg	gcc	tca	ctg	cgt	gtt	ttg	tgg	gtg	398
Val	Leu	Glu	Leu	Gly	Ala	Thr	Gly	Ala	Ser	Leu	Arg	Val	Leu	Trp	Val	
		95					100					105				
act	cta	act	ggc	att	gag	ggg	cat	agg	gtg	gag	ccc	aga	agc	cag	gag	446
Thr	Leu	Thr	Gly	Ile	Glu	Gly	His	Arg	Val	Glu	Pro	Arg	Ser	Gln	Glu	
	110					115					120					
ttt	gtg	atc	ccc	caa	gag	gtg	atg	ctg	ggc	gct	ggc	cag	cag	ctc	ttt	494
Phe	Val	Ile	Pro	Gln	Glu	Val	Met	Leu	Gly	Ala	Gly	Gln	Gln	Leu	Phe	
125					130					135					140	
gac	ttt	gct	gcc	cac	tgc	ctg	tct	gag	ttc	ctg	gat	gcg	cag	cct	gtg	542
Asp	Phe	Ala	Ala	His	Cys	Leu	Ser	Glu	Phe	Leu	Asp	Ala	Gln	Pro	Val	
				145					150					155		
aac	aaa	cag	ggc	ctg	cag	ctt	ggc	ttc	agc	ttc	tct	ttc	cct	tgt	cac	590
Asn	Lys	Gln	Gly	Leu	Gln	Leu	Gly	Phe	Ser	Phe	Ser	Phe	Pro	Cys	His	
		160					165						170			
cag	acg	ggc	ttg	gac	agg	agc	acc	ctc	att	tcc	tgg	acc	aaa	ggc	ttt	638
Gln	Thr	Gly	Leu	Asp	Arg	Ser	Thr	Leu	Ile	Ser	Trp	Thr	Lys	Gly	Phe	
		175					180					185				
agg	tgc	agt	ggc	gtg	gaa	ggc	cag	gat	gtg	gtc	cag	ctg	ctg	aga	gat	686
Arg	Cys	Ser	Gly	Val	Glu	Gly	Gln	Asp	Val	Val	Gln	Leu	Leu	Arg	Asp	
	190					195					200					
gcc	att	cgg	agg	cag	ggg	gcc	tac	aac	atc	gac	gtg	gtt	gct	gtg	gtg	734
Ala	Ile	Arg	Arg	Gln	Gly	Ala	Tyr	Asn	Ile	Asp	Val	Val	Ala	Val	Val	
205					210					215					220	
aac	gac	aca	gtg	ggc	acc	atg	atg	ggc	tgt	gag	ccg	ggg	gtc	agg	ccg	782
Asn	Asp	Thr	Val	Gly	Thr	Met	Met	Gly	Cys	Glu	Pro	Gly	Val	Arg	Pro	
				225					230					235		
tgt	gag	gtt	ggg	cta	gtt	gta	gac	acg	ggc	acc	aac	gcg	tgt	tac	atg	830
Cys	Glu	Val	Gly	Leu	Val	Val	Asp	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met	
			240					245					250			
gag	gag	gca	cgg	cat	gtg	gca	gtg	ctg	gac	gaa	gac	cgg	ggc	cgc	gtc	878
Glu	Glu	Ala	Arg	His	Val	Ala	Val	Leu	Asp	Glu	Asp	Arg	Gly	Arg	Val	
		255					260					265				
tgc	gtc	agc	gtc	gag	tgg	ggc	tcc	tta	agc	gat	gat	ggg	gcg	ctg	gga	926
Cys	Val	Ser	Val	Glu	Trp	Gly	Ser	Leu	Ser	Asp	Asp	Gly	Ala	Leu	Gly	
	270					275					280					
cca	gtg	ctg	acc	acc	ttc	gac	cat	acc	ctg	gac	cat	gag	tcc	ctg	aat	974
Pro	Val	Leu	Thr	Thr	Phe	Asp	His	Thr	Leu	Asp	His	Glu	Ser	Leu	Asn	
285					290					295					300	
cct	ggc	gct	cag	agg	ttt	gag	aag	atg	atc	gga	ggc	ctg	tac	ctg	ggc	1022
Pro	Gly	Ala	Gln	Arg	Phe	Glu	Lys	Met	Ile	Gly	Gly	Leu	Tyr	Leu	Gly	
				305					310					315		
gag	ctg	gtg	cgg	ctg	gtg	ctg	gct	cac	ttg	gcc	cgg	tgt	ggg	gtc	ctc	1070

Glu	Leu	Val	Arg	Leu	Val	Leu	Ala	His	Leu	Ala	Arg	Cys	Gly	Val	Leu	
			320					325					330			
ttt	ggt	ggc	tgc	acc	tcc	cct	gcc	ctg	ctg	agc	caa	ggc	agc	atc	ctc	1118
Phe	Gly	Gly	Cys	Thr	Ser	Pro	Ala	Leu	Leu	Ser	Gln	Gly	Ser	Ile	Leu	
			335				340					345				
ctg	gaa	cac	gtg	gct	gag	atg	gag	gag	tgagtcgggg	agatggtggt						1165
Leu	Glu	His	Val	Ala	Glu	Met	Glu	Glu								
			350				355									
ttagtggggg	attcttggct	tggaggaagg	ggatgatact	ctgttcccaa	ggtagccatg											1225
gggctttagt	gggatgggga	gcttctgggc	tgagcccaa	accacttccc	tttcccctcc											1285
agcccctcta	ctggggcagc	ccgtgtccat	gctatcctgc	aggacttggg	cctgagccct											1345
ggggcttcgg	atgttgagct	tgtgcagcac	gtctgtgcgg	ccgtgtgcac	gcggtgtgcc											1405
cagctctgtg	ctgccgccct	ggccgctgtt	ctctcctgcc	tccagcacag	ccgggagcaa											1465
caaacactcc	aggttgctgt	ggccaccgga	ggccgagtgt	gtgagcggca	ccccagggtc											1525
tgcagcgtcc	tgcaggggac	agtgatgtct	ctggccccgg	aatgcgatgt	ctccttaatc											1585
ccctctgtgg	atggtggtgg	ccggggagtg	gcgatggtga	ctgctgtggc	tgcccgtctg											1645
gctgccacc	ggcgctgct	ggaggagacc	ctggcccat	tccggttgaa	ccatgatcaa											1705
ctggctgcgg	ttcaggcaca	gatgcggaag	gcatggcca	aggggctccg	aggggaggcc											1765
tctcccttc	gcatgctgcc	cactttcgtc	cgggccaccc	ctgacggcag	cgagcgaggg											1825
gatttcttgg	ccctggacct	cgggggcacg	aacttccgtg	tctccttggt	acgtgtgacc											1885
acaggcgtgc	agatcaccag	cgagatctac	tccattcccc	agactgtggc	ccagggttct											1945
gggcagcagc	tctttgacca	catcgtggac	tgcacgtgg	acttccagca	gaagcagggc											2005
ctgagcgggc	agagcctccc	actgggtttt	accttctcct	tcccatgtag	gcagcttggc											2065
ctagaccagg	gcatcctcct	gaactggacc	aagggtttca	aggcatcaga	ctgcgagggc											2125
caagatgtcg	tgagtctgtt	gcgggaagcc	atcactcgca	gacaggcagt	ggagctgaat											2185
gtggttgcca	ttgtcaatga	cacggtgggg	accatgatgt	cctgtggcta	tgaggacccc											2245
cgttgcgaga	taggcctcat	tgtcggaacc	ggcaccaatg	cctgctacat	ggaggagctc											2305
cggaatgtgg	cgggcgtgcc	tggggactca	ggccgcatgt	gcatcaacat	ggagtggggc											2365
gcctttgggg	acgatggctc	tctggccatg	ctcagcaccc	gctttgatgc	aagtgtggac											2425
caggcgtcca	tcaaccccgg	caagcagagg	tttgaaaaga	tgatcagcgg	catgtacctg											2485
ggggagatcg	tccgccacat	ccttttacat	ttaaccagcc	ttggcgttct	cttccggggc											2545

cagcagatcc agcgccttca gaccagggac atcttcaaga ccaagttcct ctctgagatc 2605
gaaagtgaca gcctggccct gcggcaggtc cgagccatcc tagaggatct ggggctaccc 2665
ctgacctcag atgacgcctt gatggtgcta gaggtgtgcc aggtgtgtgc ccagaggggt 2725
gccagctctt gtggggcggg tgtagctgcc gtggtggaga agatccgggg gaaccggggc 2785
ctggaagagc tggcagtgtc tgtgggggtg gatggaacgc tctacaagct gcaccgcgc 2845
ttctccagcc tgggtggcgc cacagtgcgg gagctggccc ctgctgtgtt ggtcacgttc 2905
ctgcagtcag aggatgggtc cggcaaaggt gcggccctgg tcaccgctgt tgctgccc 2965
cttgccagct tgactcgtgt ctgaggaaac ctccaggctg aggaggtctc cggcgcagcc 3025
ttgctggagc cgggtcgggg tctgctgtt tcccagccag gccagccac ccaggactcc 3085
tgggacatcc catgtgtgac ccctctgcgg ccatttggcc ttgctccctg gctttccctg 3145
agagaagtag cactcaggtt agcaatatat atatataatt tatttacaaa aaaaaaaaaa 3205

<210> 44

<211> 357

<212> PRT

<213> Homo sapiens

<400> 44

Met	Asp	Ser	Ile	Gly	Ser	Ser	Gly	Leu	Arg	Gln	Gly	Glu	Glu	Thr	Leu
1				5					10					15	
Ser	Cys	Ser	Glu	Glu	Gly	Leu	Pro	Gly	Pro	Ser	Asp	Ser	Ser	Glu	Leu
			20					25					30		
Val	Gln	Glu	Cys	Leu	Gln	Gln	Phe	Lys	Val	Thr	Arg	Ala	Gln	Leu	Gln
			35				40					45			
Gln	Ile	Gln	Ala	Ser	Leu	Leu	Gly	Ser	Met	Glu	Gln	Ala	Leu	Arg	Gly
	50					55					60				
Gln	Ala	Ser	Pro	Ala	Pro	Ala	Val	Arg	Met	Leu	Pro	Thr	Tyr	Val	Gly
	65				70					75					80
Ser	Thr	Pro	His	Gly	Thr	Glu	Gln	Gly	Asp	Phe	Val	Val	Leu	Glu	Leu
				85					90					95	
Gly	Ala	Thr	Gly	Ala	Ser	Leu	Arg	Val	Leu	Trp	Val	Thr	Leu	Thr	Gly
			100					105					110		
Ile	Glu	Gly	His	Arg	Val	Glu	Pro	Arg	Ser	Gln	Glu	Phe	Val	Ile	Pro
		115					120					125			
Gln	Glu	Val	Met	Leu	Gly	Ala	Gly	Gln	Gln	Leu	Phe	Asp	Phe	Ala	Ala
		130					135					140			
His	Cys	Leu	Ser	Glu	Phe	Leu	Asp	Ala	Gln	Pro	Val	Asn	Lys	Gln	Gly
145						150				155					160

Leu Gln Leu Gly Phe Ser Phe Ser Phe Pro Cys His Gln Thr Gly Leu
 165 170 175
 Asp Arg Ser Thr Leu Ile Ser Trp Thr Lys Gly Phe Arg Cys Ser Gly
 180 185 190
 Val Glu Gly Gln Asp Val Val Gln Leu Leu Arg Asp Ala Ile Arg Arg
 195 200 205
 Gln Gly Ala Tyr Asn Ile Asp Val Val Ala Val Val Asn Asp Thr Val
 210 215 220
 Gly Thr Met Met Gly Cys Glu Pro Gly Val Arg Pro Cys Glu Val Gly
 225 230 235 240
 Leu Val Val Asp Thr Gly Thr Asn Ala Cys Tyr Met Glu Glu Ala Arg
 245 250 255
 His Val Ala Val Leu Asp Glu Asp Arg Gly Arg Val Cys Val Ser Val
 260 265 270
 Glu Trp Gly Ser Leu Ser Asp Asp Gly Ala Leu Gly Pro Val Leu Thr
 275 280 285
 Thr Phe Asp His Thr Leu Asp His Glu Ser Leu Asn Pro Gly Ala Gln
 290 295 300
 Arg Phe Glu Lys Met Ile Gly Gly Leu Tyr Leu Gly Glu Leu Val Arg
 305 310 315 320
 Leu Val Leu Ala His Leu Ala Arg Cys Gly Val Leu Phe Gly Gly Cys
 325 330 335
 Thr Ser Pro Ala Leu Leu Ser Gln Gly Ser Ile Leu Leu Glu His Val
 340 345 350
 Ala Glu Met Glu Glu
 355

<210> 45
 <211> 1096
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1096)

<400> 45
 c acc aag ctt ccc acc atg gac tcc att ggg tct tca ggg ttg cgg cag 49
 Thr Lys Leu Pro Thr Met Asp Ser Ile Gly Ser Ser Gly Leu Arg Gln
 1 5 10 15
 ggg gaa gaa acc ctg agt tgc tct gag gag ggc ttg ccc ggg ccc tca 97
 Gly Glu Glu Thr Leu Ser Cys Ser Glu Glu Gly Leu Pro Gly Pro Ser
 20 25 30

gac agc tca gag ctg gtg cag gag tgc ctg cag cag ttc aag gtg aca	145
Asp Ser Ser Glu Leu Val Gln Glu Cys Leu Gln Gln Phe Lys Val Thr	
35 40 45	
agg gca cag cta cag cag atc caa gcc agc ctc ttg ggt tcc atg gag	193
Arg Ala Gln Leu Gln Gln Ile Gln Ala Ser Leu Leu Gly Ser Met Glu	
50 55 60	
cag gcg ctg agg gga cag gcc agc cct gcc cct gcg gtc cgg atg ctg	241
Gln Ala Leu Arg Gly Gln Ala Ser Pro Ala Pro Ala Val Arg Met Leu	
65 70 75 80	
cct aca tac gtg ggg tcc acc cca cat ggc act gag caa gga gac ttc	289
Pro Thr Tyr Val Gly Ser Thr Pro His Gly Thr Glu Gln Gly Asp Phe	
85 90 95	
gtg gtg ctg gag ctg ggg gcc aca ggg gcc tca ctg cgt gtt ttg tgg	337
Val Val Leu Glu Leu Gly Ala Thr Gly Ala Ser Leu Arg Val Leu Trp	
100 105 110	
gtg act cta act ggc att gag ggg cat agg gtg gag ccc aga agc cag	385
Val Thr Leu Thr Gly Ile Glu Gly His Arg Val Glu Pro Arg Ser Gln	
115 120 125	
gag ttt gtg atc ccc caa gag gtg atg ctg ggt gct ggc cag cag ctc	433
Glu Phe Val Ile Pro Gln Glu Val Met Leu Gly Ala Gly Gln Gln Leu	
130 135 140	
ttt gac ttt gct gcc cac tgc ctg tct gag ttc ctg gat gcg cag cct	481
Phe Asp Phe Ala Ala His Cys Leu Ser Glu Phe Leu Asp Ala Gln Pro	
145 150 155 160	
gtg aac aaa cag ggt ctg cag ctt ggc ttc agc ttc tct ttc cct tgt	529
Val Asn Lys Gln Gly Leu Gln Leu Gly Phe Ser Phe Ser Phe Pro Cys	
165 170 175	
cac cag acg ggc ttg gac agg agc acc ctc att tcc tgg acc aaa ggt	577
His Gln Thr Gly Leu Asp Arg Ser Thr Leu Ile Ser Trp Thr Lys Gly	
180 185 190	
ttt agg tgc agt ggt gtg gaa ggc cag gat gtg gtc cag ctg ctg aga	625
Phe Arg Cys Ser Gly Val Glu Gly Gln Asp Val Val Gln Leu Leu Arg	
195 200 205	
gat gcc att cgg agg cag ggg gcc tac aac atc gac gtg gtt gct gtg	673
Asp Ala Ile Arg Arg Gln Gly Ala Tyr Asn Ile Asp Val Val Ala Val	
210 215 220	
gtg aac gac aca gtg ggc acc atg atg ggc tgt gag ccg ggg gtc agg	721
Val Asn Asp Thr Val Gly Thr Met Met Gly Cys Glu Pro Gly Val Arg	
225 230 235 240	
ccg tgt gag gtt ggg cta gtt gta gac acg ggc acc aac gcg tgt tac	769
Pro Cys Glu Val Gly Leu Val Val Asp Thr Gly Thr Asn Ala Cys Tyr	
245 250 255	

atg gag gag gca cgg cat gtg gca gtg ctg gac gaa gac cgg ggc cgc	817
Met Glu Glu Ala Arg His Val Ala Val Leu Asp Glu Asp Arg Gly Arg	
260 265 270	
gtc tgc gtc agc gtc gag tgg ggc tcc ttc agc gat gat ggg gcg ctg	865
Val Cys Val Ser Val Glu Trp Gly Ser Phe Ser Asp Asp Gly Ala Leu	
275 280 285	
gga cca gtg ctg acc acc ttc gac cat acc ctg gac cat gag tcc ctg	913
Gly Pro Val Leu Thr Thr Phe Asp His Thr Leu Asp His Glu Ser Leu	
290 295 300	
aat cct ggt gct cag agg ttt gag aag atg atc gga ggc ctg tac ctg	961
Asn Pro Gly Ala Gln Arg Phe Glu Lys Met Ile Gly Gly Leu Tyr Leu	
305 310 315 320	
ggg gag ctg gtg cgg ctg gtg ctg gct cac ttg gcc cgg tgt ggg gtc	1009
Gly Glu Leu Val Arg Leu Val Leu Ala His Leu Ala Arg Cys Gly Val	
325 330 335	
ctc ttt ggt ggc tgc acc tcc cct gcc ctg ctg agc caa ggc agc atc	1057
Leu Phe Gly Gly Cys Thr Ser Pro Ala Leu Leu Ser Gln Gly Ser Ile	
340 345 350	
ctc ctg gaa cac gtg gct gag atg gag gag gtc gac ggc	1096
Leu Leu Glu His Val Ala Glu Met Glu Glu Val Asp Gly	
355 360 365	
<210> 46	
<211> 365	
<212> PRT	
<213> Homo sapiens	
<400> 46	
Thr Lys Leu Pro Thr Met Asp Ser Ile Gly Ser Ser Gly Leu Arg Gln	
1 5 10 15	
Gly Glu Glu Thr Leu Ser Cys Ser Glu Glu Gly Leu Pro Gly Pro Ser	
20 25 30	
Asp Ser Ser Glu Leu Val Gln Glu Cys Leu Gln Gln Phe Lys Val Thr	
35 40 45	
Arg Ala Gln Leu Gln Gln Ile Gln Ala Ser Leu Leu Gly Ser Met Glu	
50 55 60	
Gln Ala Leu Arg Gly Gln Ala Ser Pro Ala Pro Ala Val Arg Met Leu	
65 70 75 80	
Pro Thr Tyr Val Gly Ser Thr Pro His Gly Thr Glu Gln Gly Asp Phe	
85 90 95	
Val Val Leu Glu Leu Gly Ala Thr Gly Ala Ser Leu Arg Val Leu Trp	
100 105 110	
Val Thr Leu Thr Gly Ile Glu Gly His Arg Val Glu Pro Arg Ser Gln	
115 120 125	

Glu Phe Val Ile Pro Gln Glu Val Met Leu Gly Ala Gly Gln Gln Leu
 130 135 140
 Phe Asp Phe Ala Ala His Cys Leu Ser Glu Phe Leu Asp Ala Gln Pro
 145 150 155 160
 Val Asn Lys Gln Gly Leu Gln Leu Gly Phe Ser Phe Ser Phe Pro Cys
 165 170 175
 His Gln Thr Gly Leu Asp Arg Ser Thr Leu Ile Ser Trp Thr Lys Gly
 180 185 190
 Phe Arg Cys Ser Gly Val Glu Gly Gln Asp Val Val Gln Leu Leu Arg
 195 200 205
 Asp Ala Ile Arg Arg Gln Gly Ala Tyr Asn Ile Asp Val Val Ala Val
 210 215 220
 Val Asn Asp Thr Val Gly Thr Met Met Gly Cys Glu Pro Gly Val Arg
 225 230 235 240
 Pro Cys Glu Val Gly Leu Val Val Asp Thr Gly Thr Asn Ala Cys Tyr
 245 250 255
 Met Glu Glu Ala Arg His Val Ala Val Leu Asp Glu Asp Arg Gly Arg
 260 265 270
 Val Cys Val Ser Val Glu Trp Gly Ser Phe Ser Asp Asp Gly Ala Leu
 275 280 285
 Gly Pro Val Leu Thr Thr Phe Asp His Thr Leu Asp His Glu Ser Leu
 290 295 300
 Asn Pro Gly Ala Gln Arg Phe Glu Lys Met Ile Gly Gly Leu Tyr Leu
 305 310 315 320
 Gly Glu Leu Val Arg Leu Val Leu Ala His Leu Ala Arg Cys Gly Val
 325 330 335
 Leu Phe Gly Gly Cys Thr Ser Pro Ala Leu Leu Ser Gln Gly Ser Ile
 340 345 350
 Leu Leu Glu His Val Ala Glu Met Glu Glu Val Asp Gly
 355 360 365

<210> 47

<211> 1096

<212> DNA

<213> Homo sapiens .

<220>

<221> CDS

<222> (17) .. (1087)

<400> 47

caccaagctt cccacc atg gac tcc att ggg tct tca ggg ttg cgg cag ggg 52

Met Asp Ser Ile Gly Ser Ser Gly Leu Arg Gln Gly																	
1					5					10							
gaa	gaa	acc	ctg	agt	tgc	tct	gag	gag	ggc	ttg	ccc	ggg	ccc	tca	gac	100	
Glu	Glu	Thr	Leu	Ser	Cys	Ser	Glu	Glu	Gly	Leu	Pro	Gly	Pro	Ser	Asp		
15			20					25									
agc	tca	gag	ctg	gtg	cag	gag	tgc	ctg	cag	cag	ttc	aag	gtg	aca	agg	148	
Ser	Ser	Glu	Leu	Val	Gln	Glu	Cys	Leu	Gln	Gln	Phe	Lys	Val	Thr	Arg		
30			35					40									
gca	cag	cta	cag	cag	atc	caa	gcc	agc	ctc	ttg	ggc	tcc	atg	gag	cag	196	
Ala	Gln	Leu	Gln	Gln	Ile	Gln	Ala	Ser	Leu	Leu	Gly	Ser	Met	Glu	Gln		
45			50					55							60		
gcg	ctg	agg	gga	cag	gcc	agc	cct	gcc	cct	gcg	gtc	cgg	atg	ctg	cct	244	
Ala	Leu	Arg	Gly	Gln	Ala	Ser	Pro	Ala	Pro	Ala	Val	Arg	Met	Leu	Pro		
65				70							75						
aca	tac	gtg	ggg	tcc	acc	cca	cat	ggc	act	gag	caa	gga	gac	ttc	gtg	292	
Thr	Tyr	Val	Gly	Ser	Thr	Pro	His	Gly	Thr	Glu	Gln	Gly	Asp	Phe	Val		
80				85							90						
gtg	ctg	gag	ctg	ggg	gcc	aca	ggg	gcc	tca	ctg	cgt	gtt	ttg	tgg	gtg	340	
Val	Leu	Glu	Leu	Gly	Ala	Thr	Gly	Ala	Ser	Leu	Arg	Val	Leu	Trp	Val		
95			100					105									
act	cta	act	ggc	att	gag	ggg	cat	agg	gtg	gag	ccc	aga	agc	cag	gag	388	
Thr	Leu	Thr	Gly	Ile	Glu	Gly	His	Arg	Val	Glu	Pro	Arg	Ser	Gln	Glu		
110			115					120									
ttt	gtg	atc	ccc	caa	gag	gtg	atg	ctg	ggc	gct	ggc	cag	cag	ctc	ttt	436	
Phe	Val	Ile	Pro	Gln	Glu	Val	Met	Leu	Gly	Ala	Gly	Gln	Gln	Leu	Phe		
125			130					135							140		
gac	ttt	gct	gcc	cac	tgc	ctg	tct	gag	ttc	ctg	gat	gcg	cag	cct	gtg	484	
Asp	Phe	Ala	Ala	His	Cys	Leu	Ser	Glu	Phe	Leu	Asp	Ala	Gln	Pro	Val		
145				150							155						
aac	aaa	cag	ggc	ctg	cag	ctt	ggc	ttc	agc	ttc	tct	ttc	cct	tgt	cac	532	
Asn	Lys	Gln	Gly	Leu	Gln	Leu	Gly	Phe	Ser	Phe	Ser	Phe	Pro	Cys	His		
160			165					170									
cag	acg	ggc	ttg	gac	agg	agc	acc	ctc	att	tcc	tgg	acc	aaa	ggc	ttt	580	
Gln	Thr	Gly	Leu	Asp	Arg	Ser	Thr	Leu	Ile	Ser	Trp	Thr	Lys	Gly	Phe		
175			180					185									
agg	tgc	agt	ggc	gtg	gaa	ggc	cag	gat	gtg	gtc	cag	ctg	ctg	aga	gat	628	
Arg	Cys	Ser	Gly	Val	Glu	Gly	Gln	Asp	Val	Val	Gln	Leu	Leu	Arg	Asp		
190			195					200									
gcc	att	cgg	agg	cag	ggg	gcc	tac	aac	atc	gac	gtg	gtt	gct	gtg	gtg	676	
Ala	Ile	Arg	Arg	Gln	Gly	Ala	Tyr	Asn	Ile	Asp	Val	Val	Ala	Val	Val		
205			210					215							220		
aac	gac	aca	gtg	ggc	acc	atg	atg	ggc	tgt	gag	ccg	ggg	gtc	agg	ccg	724	
Asn	Asp	Thr	Val	Gly	Thr	Met	Met	Gly	Cys	Glu	Pro	Gly	Val	Arg	Pro		

225								230					235					
tgt	gag	gtt	ggg	cta	gtt	gta	gac	acg	ggc	acc	aac	gcg	tgt	tac	atg	772		
Cys	Glu	Val	Gly	Leu	Val	Val	Asp	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met			
			240				245						250					
gag	gag	gca	cgg	cat	gtg	gca	gtg	ctg	gac	gaa	gac	cgg	ggc	cgc	gtc	820		
Glu	Glu	Ala	Arg	His	Val	Ala	Val	Leu	Asp	Glu	Asp	Arg	Gly	Arg	Val			
			255				260						265					
tgc	gtc	agc	gtc	gag	tgg	ggc	tcc	ttc	agc	gat	gat	ggg	gcg	ctg	gga	868		
Cys	Val	Ser	Val	Glu	Trp	Gly	Ser	Phe	Ser	Asp	Asp	Gly	Ala	Leu	Gly			
			270				275						280					
cca	gtg	ctg	acc	acc	ttc	gac	cat	acc	ctg	gac	cat	gag	tcc	ctg	aat	916		
Pro	Val	Leu	Thr	Thr	Phe	Asp	His	Thr	Leu	Asp	His	Glu	Ser	Leu	Asn			
			285				290						295			300		
cct	ggt	gct	cag	agg	ttt	gag	aag	atg	atc	gga	ggc	ctg	tac	ctg	ggt	964		
Pro	Gly	Ala	Gln	Arg	Phe	Glu	Lys	Met	Ile	Gly	Gly	Leu	Tyr	Leu	Gly			
			305						310						315			
gag	ctg	gtg	cgg	ctg	gtg	ctg	gct	cac	ttg	gcc	cgg	tgt	ggg	gtc	ctc	1012		
Glu	Leu	Val	Arg	Leu	Val	Leu	Ala	His	Leu	Ala	Arg	Cys	Gly	Val	Leu			
			320						325						330			
ttt	ggt	ggc	tgc	acc	tcc	cct	gcc	ctg	ctg	agc	caa	ggc	agc	atc	ctc	1060		
Phe	Gly	Gly	Cys	Thr	Ser	Pro	Ala	Leu	Leu	Ser	Gln	Gly	Ser	Ile	Leu			
			335						340						345			
ctg	gaa	cac	gtg	gct	gag	atg	gag	gag	gtc	gac	ggc					1096		
Leu	Glu	His	Val	Ala	Glu	Met	Glu	Glu										
			350			355												
<210> 48																		
<211> 357																		
<212> PRT																		
<213> Homo sapiens																		
<400> 48																		
Met	Asp	Ser	Ile	Gly	Ser	Ser	Gly	Leu	Arg	Gln	Gly	Glu	Glu	Thr	Leu			
1				5				10				15						
Ser	Cys	Ser	Glu	Glu	Gly	Leu	Pro	Gly	Pro	Ser	Asp	Ser	Ser	Glu	Leu			
			20			25						30						
Val	Gln	Glu	Cys	Leu	Gln	Gln	Phe	Lys	Val	Thr	Arg	Ala	Gln	Leu	Gln			
			35			40						45						
Gln	Ile	Gln	Ala	Ser	Leu	Leu	Gly	Ser	Met	Glu	Gln	Ala	Leu	Arg	Gly			
			50			55						60						
Gln	Ala	Ser	Pro	Ala	Pro	Ala	Val	Arg	Met	Leu	Pro	Thr	Tyr	Val	Gly			
			65			70			75			80						
Ser	Thr	Pro	His	Gly	Thr	Glu	Gln	Gly	Asp	Phe	Val	Val	Leu	Glu	Leu			
			85						90			95						

Gly	Ala	Thr	Gly	Ala	Ser	Leu	Arg	Val	Leu	Trp	Val	Thr	Leu	Thr	Gly	100	105	110
Ile	Glu	Gly	His	Arg	Val	Glu	Pro	Arg	Ser	Gln	Glu	Phe	Val	Ile	Pro	115	120	125
Gln	Glu	Val	Met	Leu	Gly	Ala	Gly	Gln	Gln	Leu	Phe	Asp	Phe	Ala	Ala	130	135	140
His	Cys	Leu	Ser	Glu	Phe	Leu	Asp	Ala	Gln	Pro	Val	Asn	Lys	Gln	Gly	145	150	155
Leu	Gln	Leu	Gly	Phe	Ser	Phe	Ser	Phe	Pro	Cys	His	Gln	Thr	Gly	Leu	165	170	175
Asp	Arg	Ser	Thr	Leu	Ile	Ser	Trp	Thr	Lys	Gly	Phe	Arg	Cys	Ser	Gly	180	185	190
Val	Glu	Gly	Gln	Asp	Val	Val	Gln	Leu	Leu	Arg	Asp	Ala	Ile	Arg	Arg	195	200	205
Gln	Gly	Ala	Tyr	Asn	Ile	Asp	Val	Val	Ala	Val	Val	Asn	Asp	Thr	Val	210	215	220
Gly	Thr	Met	Met	Gly	Cys	Glu	Pro	Gly	Val	Arg	Pro	Cys	Glu	Val	Gly	225	230	235
Leu	Val	Val	Asp	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met	Glu	Glu	Ala	Arg	245	250	255
His	Val	Ala	Val	Leu	Asp	Glu	Asp	Arg	Gly	Arg	Val	Cys	Val	Ser	Val	260	265	270
Glu	Trp	Gly	Ser	Phe	Ser	Asp	Asp	Gly	Ala	Leu	Gly	Pro	Val	Leu	Thr	275	280	285
Thr	Phe	Asp	His	Thr	Leu	Asp	His	Glu	Ser	Leu	Asn	Pro	Gly	Ala	Gln	290	295	300
Arg	Phe	Glu	Lys	Met	Ile	Gly	Gly	Leu	Tyr	Leu	Gly	Glu	Leu	Val	Arg	305	310	315
Leu	Val	Leu	Ala	His	Leu	Ala	Arg	Cys	Gly	Val	Leu	Phe	Gly	Gly	Cys	325	330	335
Thr	Ser	Pro	Ala	Leu	Leu	Ser	Gln	Gly	Ser	Ile	Leu	Leu	Glu	His	Val	340	345	350
Ala	Glu	Met	Glu	Glu												355		

<210> 49
 <211> 1602
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1599)

<400> 49

atg gct tcg acc acc acc tgc acc agg ttc acg gac gag tat cag ctt	48
Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu	
1 5 10 15	
ttc gag gag ctt gga aag ggg gca ttc tca gtg gtg aga aga tgt atg	96
Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Met	
20 25 30	
aaa att cct act gga caa gga tat gct gcc aaa att atc aac acc aaa	144
Lys Ile Pro Thr Gly Gln Gly Tyr Ala Ala Lys Ile Ile Asn Thr Lys	
35 40 45	
aag ctt tct gct agg gat cat cag aaa cta gaa aga gaa gct aga atc	192
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile	
50 55 60	
tgc cgt ctt ttg aag cac cct aat att gtg cga ctt cat gat agc ata	240
Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile	
65 70 75 80	
tca gaa gag ggc ttt cac tac ttg gtg ttt gat tta gtt act gga ggt	288
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly	
85 90 95	
gaa ctg ttt gaa gac ata gtg gca aga gaa tac tac agt gaa gct gat	336
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp	
100 105 110	
gcc agt cat tgt ata cag cag att cta gaa agt gtt aat cat tgt cac	384
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ser Val Asn His Cys His	
115 120 125	
cta aat ggc ata gtt cac agg gac ctg aag cct gag aat ttg ctt tta	432
Leu Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu	
130 135 140	
gct agc aaa tcc aag gga gca gct gtg aaa ttg gca gac ttt ggc tta	480
Ala Ser Lys Ser Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu	
145 150 155 160	
gcc ata gaa gtt caa ggg gac cag cag gcg tgg ttt ggt ttt gct ggc	528
Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly	
165 170 175	
aca cct gga tat ctt tct cca gaa gtt tta cgt aaa gat cct tat gga	576
Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly	
180 185 190	
aag cca gtg gat atg tgg gca tgt ggt gtc att ctc tat att cta ctt	624
Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu	
195 200 205	

gtg ggg tat cca ccc ttc tgg gat gaa gac caa cac aga ctc tat cag	672
Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Arg Leu Tyr Gln	
210 215 220	
cag atc aag gct gga gct tat gat ttt cca tca cca gaa tgg gac acg	720
Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr	
225 230 235 240	
gtg act cct gaa gcc aaa gac ctc atc aat aaa atg ctt act atc aac	768
Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met Leu Thr Ile Asn	
245 250 255	
cct gcc aaa cgc atc aca gcc tca gag gca ctg aag cac cca tgg atc	816
Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys His Pro Trp Ile	
260 265 270	
tgt caa cgt tct act gtt gct tcc atg atg cac aga cag gag act gta	864
Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val	
275 280 285	
gac tgc ttg aag aaa ttt aat gct aga aga aaa cta aag ggt gcc atc	912
Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile	
290 295 300	
ttg aca act atg ctg gct aca agg aat ttc tca gca gcc aag agt ttg	960
Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala Ala Lys Ser Leu	
305 310 315 320	
ttg aag aaa cca gat gga gta aag ata aac aac aaa gcc aac gtg gta	1008
Leu Lys Lys Pro Asp Gly Val Lys Ile Asn Asn Lys Ala Asn Val Val	
325 330 335	
acc agc ccc aaa gaa aat att cct acc cca gcg ctg gag ccc caa act	1056
Thr Ser Pro Lys Glu Asn Ile Pro Thr Pro Ala Leu Glu Pro Gln Thr	
340 345 350	
act gta atc cac aac cct gat gga aac aag gag tca act gag agt tca	1104
Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser	
355 360 365	
aat aca aca att gag gat gaa gat gtg aaa gca cga aag caa gag att	1152
Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile	
370 375 380	
atc aaa gtc act gaa caa ctg atc gaa gct atc aac aat ggg gac ttt	1200
Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe	
385 390 395 400	
gaa gcc tac aca aaa atc tgt gac cca ggc ctt act gct ttt gaa cct	1248
Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro	
405 410 415	
gaa gct ttg ggt aat tta gtg gaa ggg atg gat ttt cac cga ttc tac	1296
Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr	
420 425 430	
ttt gaa aat gct ttg tcc aaa agc aat aaa cca atc cac act att att	1344

Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile
435 440 445
cta aac cct cat gta cat ctg gta ggg gat gat gcc gcc tgc ata gca 1392
Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys Ile Ala
450 455 460
tat att agg ctc aca cag tac atg gat ggc agt gga atg cca aag aca 1440
Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro Lys Thr
465 470 475 480
atg cag tca gaa gag act cgt gtg tgg cac cgc cgg gat gga aag tgg 1488
Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp
485 490 495
cag aat gtt cat ttt cat cgc tcg ggg tca cca aca gta ccc atc aag 1536
Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Lys
500 505 510
cca ccc tgt att cca aat ggg aaa gaa aac ttc tca gga ggc acc tct 1584
Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly Thr Ser
515 520 525
ttg tgg caa aac atc tga 1602
Leu Trp Gln Asn Ile
530
<210> 50
<211> 533
<212> PRT
<213> Homo sapiens
<400> 50
Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp Glu Tyr Gln Leu
1 5 10 15
Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val Arg Arg Cys Met
20 25 30
Lys Ile Pro Thr Gly Gln Gly Tyr Ala Ala Lys Ile Ile Asn Thr Lys
35 40 45
Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile
50 55 60
Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile
65 70 75 80
Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly
85 90 95
Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp
100 105 110
Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ser Val Asn His Cys His
115 120 125

Leu Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
 130 135 140
 Ala Ser Lys Ser Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu
 145 150 155 160
 Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe Gly Phe Ala Gly
 165 170 175
 Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly
 180 185 190
 Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu
 195 200 205
 Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Arg Leu Tyr Gln
 210 215 220
 Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr
 225 230 235 240
 Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met Leu Thr Ile Asn
 245 250 255
 Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys His Pro Trp Ile
 260 265 270
 Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val
 275 280 285
 Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile
 290 295 300
 Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala Ala Lys Ser Leu
 305 310 315 320
 Leu Lys Lys Pro Asp Gly Val Lys Ile Asn Asn Lys Ala Asn Val Val
 325 330 335
 Thr Ser Pro Lys Glu Asn Ile Pro Thr Pro Ala Leu Glu Pro Gln Thr
 340 345 350
 Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser
 355 360 365
 Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile
 370 375 380
 Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe
 385 390 395 400
 Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro
 405 410 415
 Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr
 420 425 430

Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile
 435 440 445
 Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys Ile Ala
 450 455 460
 Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro Lys Thr
 465 470 475 480
 Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp
 485 490 495
 Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Lys
 500 505 510
 Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly Thr Ser
 515 520 525
 Leu Trp Gln Asn Ile
 530

<210> 51
 <211> 1519
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1519)

<400> 51
 c acc gga tcc acc atg gct tcg acc acc acc tgc acc agg ttc acg gac 49
 Thr Gly Ser Thr Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp
 1 5 10 15
 gag tat cag ctt ttc gag gag ctt gga aag ggg gca ttc tca gtg gtg 97
 Glu Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val
 20 25 30
 aga aga tgt atg aaa att cct act gga caa gaa tat gct gcc aaa att 145
 Arg Arg Cys Met Lys Ile Pro Thr Gly Gln Glu Tyr Ala Ala Lys Ile
 35 40 45
 atc aac acc aaa aag ctt tct gct agg gat cat cag aaa cta gaa aga 193
 Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg
 50 55 60
 gaa gct aga atc tgc cgt ctt ttg aag cac cct aat att gtg cga ctt 241
 Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu
 65 70 75 80
 cat gat agc ata tca gaa gag ggc ttt cac tac ttg gtg ttt gat tta 289
 His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu
 85 90 95
 gtt act gga ggt gaa ctg ttt gaa gac ata gtg gca aga gaa tac tac 337
 Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr

100					105					110						
agt	gaa	gct	gat	gcc	agt	cat	tgt	ata	cag	cag	att	cta	gaa	agt	gtt	385
Ser	Glu	Ala	Asp	Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ser	Val	
115					120					125						
aat	cat	tgt	cac	cta	aat	ggc	ata	gtt	cac	agg	gac	ctg	aag	cct	gag	433
Asn	His	Cys	His	Leu	Asn	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	
130					135					140						
aat	ttg	ctt	tta	gct	agc	aaa	tcc	aag	gga	gca	gct	gtg	aaa	ttg	gca	481
Asn	Leu	Leu	Leu	Ala	Ser	Lys	Ser	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	
145					150					155					160	
gac	ttt	ggc	tta	gcc	ata	gaa	gtt	caa	ggg	gac	cag	cag	gcg	tggt	ttt	529
Asp	Phe	Gly	Leu	Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	
165					170					175						
ggc	ttt	gct	ggc	aca	cct	gga	tat	ctt	tct	cca	gaa	gtt	tta	cgt	aaa	577
Gly	Phe	Ala	Gly	Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	
180					185					190						
gat	cct	tat	gga	aag	cca	gtg	gat	atg	tggt	gca	tgt	ggc	gtc	att	ctc	625
Asp	Pro	Tyr	Gly	Lys	Pro	Val	Asp	Met	Trp	Ala	Cys	Gly	Val	Ile	Leu	
195					200					205						
tat	att	cta	ctt	gtg	ggg	tat	cca	ccc	ttc	tggt	gat	gaa	gac	caa	cac	673
Tyr	Ile	Leu	Leu	Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	
210					215					220						
aga	ctc	tat	cag	cag	atc	aag	gct	gga	gct	tat	gat	ttt	cca	tca	cca	721
Arg	Leu	Tyr	Gln	Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	
225					230					235					240	
gaa	tggt	gac	acg	gtg	act	cct	gaa	gcc	aaa	gac	ctc	atc	aat	aaa	atg	769
Glu	Trp	Asp	Thr	Val	Thr	Pro	Glu	Ala	Lys	Asp	Leu	Ile	Asn	Lys	Met	
245					250					255						
ctt	act	atc	aac	cct	gcc	aaa	cgc	atc	aca	gcc	tca	gag	gca	ctg	aag	817
Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg	Ile	Thr	Ala	Ser	Glu	Ala	Leu	Lys	
260					265					270						
cac	cca	tggt	atc	tgt	caa	cgt	tct	act	gtt	gct	tcc	atg	atg	cac	aga	865
His	Pro	Trp	Ile	Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	
275					280					285						
cag	gag	act	gta	gac	tgc	ttg	aag	aaa	ttt	aat	gct	aga	aga	aaa	cta	913
Gln	Glu	Thr	Val	Asp	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	
290					295					300						
aag	ggc	gcc	atc	ttg	aca	act	atg	ctg	gct	aca	agg	aat	ttc	tca	gca	961
Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	
305					310					315					320	
gcc	aag	agt	ttg	ttg	aag	aaa	cca	gat	gga	gta	aag	gag	tca	act	gag	1009
Ala	Lys	Ser	Leu	Leu	Lys	Lys	Pro	Asp	Gly	Val	Lys	Glu	Ser	Thr	Glu	
325					330					335						

agt tca aat aca aca att gag gat gaa gat gtg aaa gca cga aag caa	1057
Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln	
340 345 350	
gag att atc aaa gtc act gaa caa ctg atc gaa gct atc aac aat ggg	1105
Glu Ile Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly	
355 360 365	
gac ttt gaa gcc tac aca aaa atc tgt gac cca ggc ctt act gct ttt	1153
Asp Phe Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe	
370 375 380	
gaa cct gaa gct ttg ggt aat tta gtg gaa ggg atg gat ttt cac cga	1201
Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg	
385 390 395 400	
ttc tac ttt gaa aat gct ttg tcc aaa agc aat aaa cca atc cac act	1249
Phe Tyr Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr	
405 410 415	
att att cta aac cct cat gta cat ctg gta ggg gat gat gcc gcc tgc	1297
Ile Ile Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys	
420 425 430	
ata gca tat att agg ctc aca cag tac atg gat ggc agt gga atg cca	1345
Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro	
435 440 445	
aag aca atg cag tca gaa gag act cgt gtg tgg cac cgc cgg gat gga	1393
Lys Thr Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly	
450 455 460	
aag tgg cag aat gtt cat ttt cat cgc tcg ggg tca cca aca gta ccc	1441
Lys Trp Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro	
465 470 475 480	
atc aag cca ccc tgt att cca aat ggg aaa gaa aac ttc tca gga ggc	1489
Ile Lys Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly	
485 490 495	
acc tct ttg tgg caa aac atc ctc gag ggc	1519
Thr Ser Leu Trp Gln Asn Ile Leu Glu Gly	
500 505	
<210> 52	
<211> 506	
<212> PRT	
<213> Homo sapiens	
<400> 52	
Thr Gly Ser Thr Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp	
1 5 10 15	
Glu Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val	
20 25 30	

Arg	Arg	Cys	Met	Lys	Ile	Pro	Thr	Gly	Gln	Glu	Tyr	Ala	Ala	Lys	Ile	35	40	45	
Ile	Asn	Thr	Lys	Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	50	55	60	
Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lys	His	Pro	Asn	Ile	Val	Arg	Leu	65	70	75	80
His	Asp	Ser	Ile	Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	85	90	95	
Val	Thr	Gly	Gly	Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	100	105	110	
Ser	Glu	Ala	Asp	Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ser	Val	115	120	125	
Asn	His	Cys	His	Leu	Asn	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	130	135	140	
Asn	Leu	Leu	Leu	Ala	Ser	Lys	Ser	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	145	150	155	160
Asp	Phe	Gly	Leu	Ala	Ile	Glu	Val	Gln	Gly	Asp	Gln	Gln	Ala	Trp	Phe	165	170	175	
Gly	Phe	Ala	Gly	Thr	Pro	Gly	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Arg	Lys	180	185	190	
Asp	Pro	Tyr	Gly	Lys	Pro	Val	Asp	Met	Trp	Ala	Cys	Gly	Val	Ile	Leu	195	200	205	
Tyr	Ile	Leu	Leu	Val	Gly	Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	210	215	220	
Arg	Leu	Tyr	Gln	Gln	Ile	Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	225	230	235	240
Glu	Trp	Asp	Thr	Val	Thr	Pro	Glu	Ala	Lys	Asp	Leu	Ile	Asn	Lys	Met	245	250	255	
Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg	Ile	Thr	Ala	Ser	Glu	Ala	Leu	Lys	260	265	270	
His	Pro	Trp	Ile	Cys	Gln	Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	275	280	285	
Gln	Glu	Thr	Val	Asp	Cys	Leu	Lys	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	290	295	300	
Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met	Leu	Ala	Thr	Arg	Asn	Phe	Ser	Ala	305	310	315	320
Ala	Lys	Ser	Leu	Leu	Lys	Lys	Pro	Asp	Gly	Val	Lys	Glu	Ser	Thr	Glu	325	330	335	

Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln
 340 345 350
 Glu Ile Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly
 355 360 365
 Asp Phe Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe
 370 375 380
 Glu Pro Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg
 385 390 395 400
 Phe Tyr Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr
 405 410 415
 Ile Ile Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys
 420 425 430
 Ile Ala Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro
 435 440 445
 Lys Thr Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly
 450 455 460
 Lys Trp Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro
 465 470 475 480
 Ile Lys Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly
 485 490 495
 Thr Ser Leu Trp Gln Asn Ile Leu Glu Gly
 500 505

<210> 53
 <211> 1561
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1561)

<400> 53
 c acc gga tcc acc atg gct tcg acc acc acc tgc acc agg ttc acg gac 49
 Thr Gly Ser Thr Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp
 1 5 10 15
 gag tat cag ctt ttc gag gag ctt gga aag ggg gca ttc tca gtg gtg 97
 Glu Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val
 20 25 30
 aga aga tgt atg aaa att cct act gga caa gaa tat gct gcc aaa att 145
 Arg Arg Cys Met Lys Ile Pro Thr Gly Gln Glu Tyr Ala Ala Lys Ile
 35 40 45
 atc aac acc aaa aag ctt tct gct agg gat cat cag aaa cta gaa aga 193
 Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg

50	55	60	
gaa gct aga atc tgc cgt ctt ttg aag cac cct aat att gtg cga ctt			241
Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu			
65	70	75	80
cat gat agc ata tca gaa gag ggc ttt cac tac ttg gtg ttt gat tta			289
His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu			
	85	90	95
gtt act gga ggt gaa ctg ttt gaa gac ata gtg gca aga gaa tac tac			337
Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr			
	100	105	110
agt gaa gct gat gcc agt cat tgt ata cag cag att cta gaa agt gtt			385
Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ser Val			
	115	120	125
aat cat tgt cac cta aat ggc ata gtt cac agg gac ctg aag cct gag			433
Asn His Cys His Leu Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu			
	130	135	140
aat ttg ctt tta gct agc aaa tcc aag gga gca gct gtg aaa ttg gca			481
Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala Val Lys Leu Ala			
	145	150	155
gac ttt ggc tta gcc ata gaa gtt caa ggg gac cag cag gcg tgg ttt			529
Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe			
	165	170	175
ggc ttt gct ggc aca cct gga tat ctt tct cca gaa gtt tta cgt aaa			577
Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys			
	180	185	190
gat cct tat gga aag cca gtg gat atg tgg gca tgt ggt gtc att ctc			625
Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu			
	195	200	205
tat att cta ctt gtg ggg tat cca ccc ttc tgg gat gaa gac caa cac			673
Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His			
	210	215	220
aga ctc tat cag cag atc aag gct gga gct tat gat ttt cca tca cca			721
Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro			
	225	230	235
gaa tgg gac acg gtg act cct gaa gcc aaa gac ctc atc aat aaa atg			769
Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met			
	245	250	255
ctt act atc aac cct gcc aaa cgc atc aca gcc tca gag gca ctg aag			817
Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys			
	260	265	270
cac cca tgg atc tgt caa cgt tct act gtt gct tcc atg atg cac aga			865
His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg			
	275	280	285

cag gag act gta gac tgc ttg aag aaa ttt aat gct aga aga aaa cta	913
Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu	
290 295 300	
aag ggt gcc atc ttg aca act atg ctg gct aca agg aat ttc tca gca	961
Lys Gly Ala Ile Leu Thr Met Leu Ala Thr Arg Asn Phe Ser Ala	
305 310 315 320	
gcc aag agt ttg ttg aag aaa cca gat gga gta aag gag ccc caa act	1009
Ala Lys Ser Leu Leu Lys Lys Pro Asp Gly Val Lys Glu Pro Gln Thr	
325 330 335	
act gta atc cac aac cct gat gga aac aag gag tca act gag agt tca	1057
Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser	
340 345 350	
aat aca aca att gag gat gaa gat gtg aaa gca cga aag caa gag att	1105
Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile	
355 360 365	
atc aaa gtc act gaa caa ctg atc gaa gct atc aac aat ggg gac ttt	1153
Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe	
370 375 380	
gaa gcc tac aca aaa atc tgt gac cca ggc ctt act gct ttt gaa cct	1201
Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro	
385 390 395 400	
gaa gct ttg ggt aat tta gtg gaa ggg atg gat ttt cac cga ttc tac	1249
Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr	
405 410 415	
ttt gaa aat gct ttg tcc aaa agc aat aaa cca atc cac act att att	1297
Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile	
420 425 430	
cta aac cct cat gta cat ctg gta ggg gat gat gcc gcc tgc ata gca	1345
Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys Ile Ala	
435 440 445	
tat att agg ctc aca cag tac atg gat ggc agt gga atg cca aag aca	1393
Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro Lys Thr	
450 455 460	
atg cag tca gaa gag act cgt gtg tgg cac cgc cgg gat gga aag tgg	1441
Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp	
465 470 475 480	
cag aat gtt cat ttt cat cgc tcg ggg tca cca aca gta ccc atc aag	1489
Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Lys	
485 490 495	
cca ccc tgt att cca aat ggg aaa gaa aac ttc tca gga ggc acc tct	1537
Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly Thr Ser	
500 505 510	

ttg tgg caa aac atc ctc gag ggc
 Leu Trp Gln Asn Ile Leu Glu Gly
 515 520

1561

<210> 54
 <211> 520
 <212> PRT
 <213> Homo sapiens

<400> 54
 Thr Gly Ser Thr Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp
 1 5 10 15
 Glu Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val
 20 25 30
 Arg Arg Cys Met Lys Ile Pro Thr Gly Gln Glu Tyr Ala Ala Lys Ile
 35 40 45
 Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg
 50 55 60
 Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu
 65 70 75 80
 His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu
 85 90 95
 Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr
 100 105 110
 Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ser Val
 115 120 125
 Asn His Cys His Leu Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu
 130 135 140
 Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala Val Lys Leu Ala
 145 150 155 160
 Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe
 165 170 175
 Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys
 180 185 190
 Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu
 195 200 205
 Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His
 210 215 220
 Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro
 225 230 235 240
 Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met
 245 250 255

Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys
 260 265 270
 His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg
 275 280 285
 Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu
 290 295 300
 Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala
 305 310 315 320
 Ala Lys Ser Leu Leu Lys Lys Pro Asp Gly Val Lys Glu Pro Gln Thr
 325 330 335
 Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser
 340 345 350
 Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile
 355 360 365
 Ile Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe
 370 375 380
 Glu Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro
 385 390 395 400
 Glu Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr
 405 410 415
 Phe Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile
 420 425 430
 Leu Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys Ile Ala
 435 440 445
 Tyr Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro Lys Thr
 450 455 460
 Met Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp
 465 470 475 480
 Gln Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Lys
 485 490 495
 Pro Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly Thr Ser
 500 505 510
 Leu Trp Gln Asn Ile Leu Glu Gly
 515 520

<210> 55
 <211> 1558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1558)

<400> 55

```

c acc gga tcc acc atg gct tcg acc acc acc tgc acc agg ttc acg gac 49
  Thr Gly Ser Thr Met Ala Ser Thr Thr Thr Cys Thr Arg Phe Thr Asp
    1             5             10             15

gag tat cag ctt ttc gag gag ctt gga aag ggg gca ttc tca gtg gtg 97
Glu Tyr Gln Leu Phe Glu Glu Leu Gly Lys Gly Ala Phe Ser Val Val
    20             25             30

aga aga tgt atg aaa att cct act gga caa gaa tat gct gcc aaa att 145
Arg Arg Cys Met Lys Ile Pro Thr Gly Gln Glu Tyr Ala Ala Lys Ile
    35             40             45

atc aac acc aaa aag ctt tct gct agg gat cat cag aaa cta gaa aga 193
Ile Asn Thr Lys Lys Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg
    50             55             60

gaa gct aga atc tgc cgt ctt ttg aag cac cct aat att gtg cga ctt 241
Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu
    65             70             75             80

cat gat agc ata tca gaa gag ggc ttt cac tac ttg gtg ttt gat tta 289
His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr Leu Val Phe Asp Leu
    85             90             95

gtt act gga ggt gaa ctg ttt gaa gac ata gtg gca aga gaa tac tac 337
Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr
    100            105            110

agt gaa gct gat gcc agt cat tgt ata cag cag att cta gaa agt gtt 385
Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile Leu Glu Ser Val
    115            120            125

aat cat tgt cac cta aat ggc ata gtt cac agg gac ctg aag cct gag 433
Asn His Cys His Leu Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu
    130            135            140

aat ttg ctt tta gct agc aaa tcc aag gga gca gct gtg aaa ttg gca 481
Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala Val Lys Leu Ala
    145            150            155            160

gac ttt ggc tta gcc ata gaa gtt caa ggg gac cag cag gcg tgg ttt 529
Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe
    165            170            175

ggg ttt gct ggc aca cct gga tat ctt tct cca gaa gtt tta cgt aaa 577
Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys
    180            185            190

gat cct tat gga aag cca gtg gat atg tgg gca tgt ggt gtc att ctc 625
Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu
    195            200            205

```

tat att cta ctt gtg ggg tat cca ccc ttc tgg gat gaa gac caa cac	673
Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His	
210 215 220	
aga ctc tat cag cag atc aag gct gga gct tat gat ttt cca tca cca	721
Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro	
225 230 235 240	
gaa tgg gac acg gtg act cct gaa gcc aaa gac ctc atc aat aaa atg	769
Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met	
245 250 255	
ctt act atc aac cct gcc aaa cgc atc aca gcc tca gag gca ctg aag	817
Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys	
260 265 270	
cac cca tgg atc tgt caa cgt tct act gtt gct tcc atg atg cac aga	865
His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg	
275 280 285	
cag gag act gta gac tgc ttg aag aaa ttt aat gct aga aga aaa cta	913
Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu	
290 295 300	
aag ggt gcc atc ttg aca act atg ctg gct aca agg aat ttc tca gcc	961
Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala	
305 310 315 320	
aag agt ttg ttg aag aaa cca gat gga gta aag gag ccc caa act act	1009
Lys Ser Leu Leu Lys Lys Pro Asp Gly Val Lys Glu Pro Gln Thr Thr	
325 330 335	
gta atc cac aac cct gat gga aac aag gag tca act gag agt tca aat	1057
Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser Asn	
340 345 350	
aca aca att gag gat gaa gat gtg aaa gca cga aag caa gag att atc	1105
Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile Ile	
355 360 365	
aaa gtc act gaa caa ctg atc gaa gct atc aac aat ggg gac ttt gaa	1153
Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu	
370 375 380	
gcc tac aca aaa atc tgt gac cca ggc ctt act gct ttt gaa cct gaa	1201
Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro Glu	
385 390 395 400	
gct ttg ggt aat tta gtg gaa ggg atg gat ttt cac cga ttc tac ttt	1249
Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe	
405 410 415	
gaa aat gct ttg tcc aaa agc aat aaa cca atc cac act att att cta	1297
Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile Leu	
420 425 430	
aac cct cat gta cat ctg gta ggg gat gat gcc gcc tgc ata gca tat	1345

Asn	Pro	His	Val	His	Leu	Val	Gly	Asp	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	
		435					440					445				
att	agg	ctc	aca	cag	tac	atg	gat	ggc	agt	gga	atg	cca	aag	aca	atg	1393
Ile	Arg	Leu	Thr	Gln	Tyr	Met	Asp	Gly	Ser	Gly	Met	Pro	Lys	Thr	Met	
		450				455				460						
cag	tca	gaa	gag	act	cgt	gtg	tgg	cac	cgc	cgg	gat	gga	aag	tgg	cag	1441
Gln	Ser	Glu	Glu	Thr	Arg	Val	Trp	His	Arg	Arg	Asp	Gly	Lys	Trp	Gln	
		465			470				475					480		
aat	gtt	cat	ttt	cat	cgc	tcg	ggg	tca	cca	aca	gta	ccc	atc	aag	cca	1489
Asn	Val	His	Phe	His	Arg	Ser	Gly	Ser	Pro	Thr	Val	Pro	Ile	Lys	Pro	
				485				490						495		
ccc	tgt	att	cca	aat	ggg	aaa	gaa	aac	ttc	tca	gga	ggc	acc	tct	ttg	1537
Pro	Cys	Ile	Pro	Asn	Gly	Lys	Glu	Asn	Phe	Ser	Gly	Gly	Thr	Ser	Leu	
			500				505						510			
tgg	caa	aac	atc	ctc	gag	ggc										1558
Trp	Gln	Asn	Ile	Leu	Glu	Gly										
		515														
<210> 56																
<211> 519																
<212> PRT																
<213> Homo sapiens																
<400> 56																
Thr	Gly	Ser	Thr	Met	Ala	Ser	Thr	Thr	Thr	Cys	Thr	Arg	Phe	Thr	Asp	
1				5					10					15		
Glu	Tyr	Gln	Leu	Phe	Glu	Glu	Leu	Gly	Lys	Gly	Ala	Phe	Ser	Val	Val	
			20					25					30			
Arg	Arg	Cys	Met	Lys	Ile	Pro	Thr	Gly	Gln	Glu	Tyr	Ala	Ala	Lys	Ile	
		35				40						45				
Ile	Asn	Thr	Lys	Lys	Leu	Ser	Ala	Arg	Asp	His	Gln	Lys	Leu	Glu	Arg	
	50				55					60						
Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lys	His	Pro	Asn	Ile	Val	Arg	Leu	
65				70					75					80		
His	Asp	Ser	Ile	Ser	Glu	Glu	Gly	Phe	His	Tyr	Leu	Val	Phe	Asp	Leu	
				85				90						95		
Val	Thr	Gly	Gly	Glu	Leu	Phe	Glu	Asp	Ile	Val	Ala	Arg	Glu	Tyr	Tyr	
		100					105						110			
Ser	Glu	Ala	Asp	Ala	Ser	His	Cys	Ile	Gln	Gln	Ile	Leu	Glu	Ser	Val	
	115					120						125				
Asn	His	Cys	His	Leu	Asn	Gly	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	
130					135						140					
Asn	Leu	Leu	Leu	Ala	Ser	Lys	Ser	Lys	Gly	Ala	Ala	Val	Lys	Leu	Ala	

145		150		155		160
Asp Phe Gly Leu	Ala Ile Glu Val Gln Gly Asp Gln Gln Ala Trp Phe					
	165			170		175
Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys						
	180			185		190
Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys Gly Val Ile Leu						
	195			200		205
Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp Glu Asp Gln His						
	210			215		220
Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro						
	225			230		235
Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu Ile Asn Lys Met						
	245			250		255
Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser Glu Ala Leu Lys						
	260			265		270
His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser Met Met His Arg						
	275			280		285
Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala Arg Arg Lys Leu						
	290			295		300
Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser Ala						
	305			310		315
Lys Ser Leu Leu Lys Lys Pro Asp Gly Val Lys Glu Pro Gln Thr Thr						
	325			330		335
Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr Glu Ser Ser Asn						
	340			345		350
Thr Thr Ile Glu Asp Glu Asp Val Lys Ala Arg Lys Gln Glu Ile Ile						
	355			360		365
Lys Val Thr Glu Gln Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu						
	370			375		380
Ala Tyr Thr Lys Ile Cys Asp Pro Gly Leu Thr Ala Phe Glu Pro Glu						
	385			390		395
Ala Leu Gly Asn Leu Val Glu Gly Met Asp Phe His Arg Phe Tyr Phe						
	405			410		415
Glu Asn Ala Leu Ser Lys Ser Asn Lys Pro Ile His Thr Ile Ile Leu						
	420			425		430
Asn Pro His Val His Leu Val Gly Asp Asp Ala Ala Cys Ile Ala Tyr						
	435			440		445
Ile Arg Leu Thr Gln Tyr Met Asp Gly Ser Gly Met Pro Lys Thr Met						

450		455		460	
Gln Ser Glu Glu Thr Arg Val Trp His Arg Arg Asp Gly Lys Trp Gln					
465		470		475	480
Asn Val His Phe His Arg Ser Gly Ser Pro Thr Val Pro Ile Lys Pro					
	485		490		495
Pro Cys Ile Pro Asn Gly Lys Glu Asn Phe Ser Gly Gly Thr Ser Leu					
	500		505		510
Trp Gln Asn Ile Leu Glu Gly					
	515				
<210> 57					
<211> 1390					
<212> DNA					
<213> Homo sapiens					
<220>					
<221> CDS					
<222> (3)..(1376)					
<400> 57					
ca ccg aat tcc acc atg ggg tgc atg aag tcc aag ttc ctc cag gtc					47
Pro Asn Ser Thr Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val					
1		5		10	15
gga ggc aat aca ttc tca aaa act gaa acc agc gcc agt gca cac tgt					95
Gly Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Ala His Cys					
	20		25		30
cct gtg tac gtg ccg gat ccc aca tcc acc atc aag ccg ggg cct aat					143
Pro Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn					
	35		40		45
agc cac aac agc aac aca cca gga atc agg gag gca ggc tct gag gac					191
Ser His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp					
	50		55		60
atc atc gtg gtt gcc ctg tac gat tac gag gcc att cac cac gaa gac					239
Ile Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp					
	65		70		75
ctc agc ttc cag aag ggg gac cag atg gtg gtc cta gag gaa tcc ggg					287
Leu Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly					
	80		85		90
gag tgg tgg aag gct cga tcc ctg gcc acc cgg aag gag ggc tac atc					335
Glu Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile					
	100		105		110
cca agc aac tat gtc gcc cgc gtt gac tct ctg gag aca gag gag tgg					383
Pro Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp					
	115		120		125
ttt ttc aag ggc atc agc cgg aag gac gca gag cgc caa ctg ctg gct					431

Phe	Phe	Lys	Gly	Ile	Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	
		130					135					140				
ccc	ggc	aac	atg	ctg	ggc	tcc	ttc	atg	atc	cgg	gat	agc	gag	acc	act	479
Pro	Gly	Asn	Met	Leu	Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	
		145				150					155					
aaa	gga	agc	tac	tct	ttg	tcc	gtg	cga	gac	tac	gac	cct	cgg	cag	gga	527
Lys	Gly	Ser	Tyr	Ser	Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	
160					165					170					175	
gat	acc	gtg	aaa	cat	tac	aag	atc	cgg	acc	ctg	gac	aac	ggg	ggc	ttc	575
Asp	Thr	Val	Lys	His	Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	
				180					185					190		
tac	ata	tcc	ccc	cga	agc	acc	ttc	agc	act	ctg	cag	gag	ctg	gtg	gac	623
Tyr	Ile	Ser	Pro	Arg	Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	
			195					200					205			
cac	tac	aag	acc	acc	tac	aac	aag	cac	acc	aag	gtg	gca	gtg	aag	acg	671
His	Tyr	Lys	Thr	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	
		210					215					220				
atg	aag	cca	ggg	agc	atg	tcg	gtg	gag	gcc	ttc	ctg	gca	gag	gcc	aac	719
Met	Lys	Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	
		225				230					235					
gtg	atg	aaa	act	ctg	cag	cat	gac	aag	ctg	gtc	aaa	ctt	cat	gcg	gtg	767
Val	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	
240					245				250						255	
gtc	acc	aag	gag	ccc	atc	tac	atc	atc	acg	gag	ttc	atg	gcc	aaa	gga	815
Val	Thr	Lys	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Ala	Lys	Gly	
				260					265					270		
agc	ttg	ctg	gac	ttt	ctg	aaa	agt	gat	gag	ggc	agc	aag	cag	cca	ttg	863
Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly	Ser	Lys	Gln	Pro	Leu	
			275					280					285			
cca	aaa	ctc	att	gac	ttc	tca	gcc	cag	att	gca	gaa	ggc	atg	gcc	ttc	911
Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Phe	
		290					295					300				
atc	gag	cag	agg	aac	tac	atc	cac	cga	gac	ctc	cga	gct	gcc	aac	atc	959
Ile	Glu	Gln	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	
		305				310					315					
ttg	gtc	tct	gca	tcc	ctg	gtg	tgt	aag	att	gct	gac	ttt	ggc	ctg	gcc	1007
Leu	Val	Ser	Ala	Ser	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	
320					325					330					335	
cgg	gtc	att	gag	gac	aac	gag	tac	acg	gct	cgg	gaa	ggg	gcc	aag	ttc	1055
Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Glu	Gly	Ala	Lys	Phe	
				340				345					350			
ccc	atc	aag	tgg	aca	gct	cct	gaa	gcc	atc	aac	ttt	ggc	tcc	ttc	acc	1103
Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Phe	Gly	Ser	Phe	Thr	

355	360	365	
atc aag tca gac gtc tgg tcc ttt ggt atc ctg ctg atg gag atc gtc			1151
Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val			
370	375	380	
acc tac ggc cgg atc cct tac cca ggg atg tca aac cct gaa gtg atc			1199
Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile			
385	390	395	
cga gct ctg gag cgt gga tac cgg atg cct cgc cca gag aac tgc cca			1247
Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro			
400	405	410	415
gag gag ctc tac aac atc atg atg cgc tgc tgg aaa aac cgt ccg gag			1295
Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu			
420	425	430	
gag cgg ccg acc ttc gaa tac atc cag agt gtg ctg gat gac ttc tac			1343
Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr			
435	440	445	
acg gcc aca gag agc cag tac caa cag cag cca tgagcggccg ctat			1390
Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro			
450	455		
<210> 58			
<211> 458			
<212> PRT			
<213> Homo sapiens			
<400> 58			
Pro Asn Ser Thr Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly			
1	5	10	15
Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Ala His Cys Pro			
20	25	30	
Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser			
35	40	45	
His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile			
50	55	60	
Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu			
65	70	75	80
Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu			
85	90	95	
Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro			
100	105	110	
Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe			
115	120	125	
Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro			

130				135				140							
Gly	Asn	Met	Leu	Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys
145					150					155					160
Gly	Ser	Tyr	Ser	Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp
				165					170					175	
Thr	Val	Lys	His	Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr
			180					185					190		
Ile	Ser	Pro	Arg	Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His
		195					200					205			
Tyr	Lys	Thr	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met
	210					215					220				
Lys	Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val
225					230					235					240
Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val
			245						250					255	
Thr	Lys	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Ala	Lys	Gly	Ser
			260					265					270		
Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly	Ser	Lys	Gln	Pro	Leu	Pro
		275					280					285			
Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Phe	Ile
	290					295					300				
Glu	Gln	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu
305					310					315					320
Val	Ser	Ala	Ser	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg
			325						330					335	
Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Glu	Gly	Ala	Lys	Phe	Pro
			340					345					350		
Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Phe	Gly	Ser	Phe	Thr	Ile
		355					360					365			
Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Met	Glu	Ile	Val	Thr
		370				375					380				
Tyr	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Ser	Asn	Pro	Glu	Val	Ile	Arg
385					390					395					400
Ala	Leu	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Arg	Pro	Glu	Asn	Cys	Pro	Glu
			405						410					415	
Glu	Leu	Tyr	Asn	Ile	Met	Met	Arg	Cys	Trp	Lys	Asn	Arg	Pro	Glu	Glu
			420						425				430		
Arg	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Val	Leu	Asp	Asp	Phe	Tyr	Thr

435 440 445

Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
450 455

<210> 59
<211> 1926
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (76)..(1590)

<400> 59
gaattccttt ctaaaatcca accattccag gaaatagaaa tatcaacttg ggggcttcc 60

gagaatgtca gattg atg ggg tgc atg aag tcc aag ttc ctc cag gtc gga 111
Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
1 5 10

ggc aat aca ttc tca aaa act gaa acc agc gcc agc cca cac tgt cct 159
Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro
15 20 25

gtg tac gtg ccg gat ccc aca tcc acc atc aag ccg ggg cct aat agc 207
Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser
30 35 40

cac aac agc aac aca cca gga atc agg gag gca ggc tct gag gac atc 255
His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile
45 50 55 60

atc gtg gtt gcc ctg tat gat tac gag gcc att cac cac gaa gac ctc 303
Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu
65 70 75

agc ttc cag aag ggg gac cag atg gtg gtc cta gag gaa tcc ggg gag 351
Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu
80 85 90

tgg tgg aag gct cga tcc ctg gcc acc cgg aag gag ggc tac atc cca 399
Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro
95 100 105

agc aac tat gtc gcc cgc gtt gac tct ctg gag aca gag gag tgg ttt 447
Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe
110 115 120

ttc aag ggc atc agc cgg aag gac gca gag cgc caa ctg ctg gct ccc 495
Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
125 130 135 140

ggc aac atg ctg ggc tcc ttc atg atc cgg gat agc gag acc act aaa 543
Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys
145 150 155

gga agc tac tct ttg tcc gtg cga gac tac gac cct cgg cag gga gat	591
Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp	
160 165 170	
acc gtg aaa cat tac aag atc cgg acc ctg gac aac ggg ggc ttc tac	639
Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr	
175 180 185	
ata tcc ccc cga agc acc ttc agc act ctg cag gag ctg gtg gac cac	687
Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His	
190 195 200	
tac aag aag ggg aac gac ggg ctc tgc cag aaa ctg tcg gtg ccc tgc	735
Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys	
205 210 215 220	
atg tct tcc aag ccc cag aag cct tgg gag aaa gat gcc tgg gag atc	783
Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile	
225 230 235	
cct cgg gaa tcc ctc aag ctg gag aag aaa ctt gga gct ggg cag ttt	831
Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe	
240 245 250	
ggg gaa gtc tgg atg gcc acc tac aac aag cac acc aag gtg gca gtg	879
Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val	
255 260 265	
aag acg atg aag cca ggg agc atg tcg gtg gag gcc ttc ctg gca gag	927
Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu	
270 275 280	
gcc aac gtg atg aaa act ctg cag cat gac aag ctg gtc aaa ctt cat	975
Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His	
285 290 295 300	
gcg gtg gtc acc aag gag ccc atc tac atc atc acg gag ttc atg gcc	1023
Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala	
305 310 315	
aaa gga agc ttg ctg gac ttt ctg aaa agt gat gag ggc agc aag cag	1071
Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln	
320 325 330	
cca ttg cca aaa ctc att gac ttc tca gcc cag att gca gaa ggc atg	1119
Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met	
335 340 345	
gcc ttc atc gag cag agg aac tac atc cac cga gac ctc cga gct gcc	1167
Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala	
350 355 360	
aac atc ttg gtc tct gca tcc ctg gtg tgt aag att gct gac ttt ggc	1215
Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly	
365 370 375 380	
ctg gcc cgg gtc att gag gac aac gag tac acg gct cgg gaa ggg gcc	1263

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395
 aag ttc ccc atc aag tgg aca gct cct gaa gcc atc aac ttt ggc tcc 1311
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser
 400 405 410
 ttc acc atc aag tca gac gtc tgg tcc ttt ggt atc ctg ctg atg gag 1359
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
 415 420 425
 atc gtc acc tac ggc cgg atc cct tac cca ggg atg tca aac cct gaa 1407
 Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu
 430 435 440
 gtg atc cga gct ctg gag cgt gga tac cgg atg cct cgc cca gag aac 1455
 Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn
 445 450 455 460
 tgc cca gag gag ctg tac aac atc atg atg cgc tgc tgg aaa aac cgt 1503
 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg
 465 470 475
 ccg gag gag cgg ccg acc ttc gaa tac atc cag agt gtg ctg gat gac 1551
 Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
 480 485 490
 ttc tac acg gcc aca gag agc cag tac caa cag cag cca tgatagggag 1600
 Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 495 500 505
 gaccagggca gggcaggggg tgcccaggtg gtggctgcaa ggtgggtcca gcaccatccg 1660
 ccagggccca cacccttc ctccaccag acaccaccc tcgcttcagg ccacagtttc 1720
 ctcatctgtc cagtgggtag gttggactgg aaaatctctt tttgactctt gcaatggaca 1780
 atctgacatt ctccaggaagc cccaagttg atatttctat ttcttggaat gggttgattt 1840
 tagttacagc tgtgatttgg aagggaaact ttcaaatag tgaaatgaat atttaaataa 1900
 aagatataaa tgccaaagtc ttacc 1926
 <210> 60
 <211> 505
 <212> PRT
 <213> Homo sapiens
 <400> 60
 Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
 1 5 10 15
 Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
 20 25 30
 Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
 35 40 45

Thr	Pro	Gly	Ile	Arg	Glu	Ala	Gly	Ser	Glu	Asp	Ile	Ile	Val	Val	Ala	
	50					55					60					
Leu	Tyr	Asp	Tyr	Glu	Ala	Ile	His	His	Glu	Asp	Leu	Ser	Phe	Gln	Lys	
	65				70					75					80	
Gly	Asp	Gln	Met	Val	Val	Leu	Glu	Glu	Ser	Gly	Glu	Trp	Trp	Lys	Ala	
				85					90					95		
Arg	Ser	Leu	Ala	Thr	Arg	Lys	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	
			100					105					110			
Ala	Arg	Val	Asp	Ser	Leu	Glu	Thr	Glu	Glu	Trp	Phe	Phe	Lys	Gly	Ile	
		115					120					125				
Ser	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ala	Pro	Gly	Asn	Met	Leu	
	130					135					140					
Gly	Ser	Phe	Met	Ile	Arg	Asp	Ser	Glu	Thr	Thr	Lys	Gly	Ser	Tyr	Ser	
	145				150					155					160	
Leu	Ser	Val	Arg	Asp	Tyr	Asp	Pro	Arg	Gln	Gly	Asp	Thr	Val	Lys	His	
				165					170					175		
Tyr	Lys	Ile	Arg	Thr	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Ile	Ser	Pro	Arg	
			180					185					190			
Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His	Tyr	Lys	Lys	Gly	
		195					200					205				
Asn	Asp	Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Met	Ser	Ser	Lys	
	210					215					220					
Pro	Gln	Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	
	225				230					235					240	
Leu	Lys	Leu	Glu	Lys	Lys	Leu	Gly	Ala	Gly	Gln	Phe	Gly	Glu	Val	Trp	
				245					250					255		
Met	Ala	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	
			260					265					270			
Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val	Met	
		275					280					285				
Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val	Thr	
	290					295					300					
Lys	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Ala	Lys	Gly	Ser	Leu	
	305				310					315					320	
Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly	Ser	Lys	Gln	Pro	Leu	Pro	Lys	
				325					330					335		
Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Phe	Ile	Glu	
			340					345					350			

Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365
 Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380
 Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400
 Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
 405 410 415
 Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
 420 425 430
 Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
 435 440 445
 Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
 450 455 460
 Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
 465 470 475 480
 Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
 485 490 495
 Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 500 505

<210> 61
 <211> 3109
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(1478)

<400> 61
 aggggctgag gaggtactgg aaaagaaaga ggagcaggag ctggaggaag acgtggagga 60
 ggagctggag gagg atg aag aga agg agt ggg acg ccc aca acc ctg tgt 110
 Met Lys Arg Arg Ser Gly Thr Pro Thr Thr Leu Cys
 1 5 10
 aag gag ctc aag tac tcc aag gac ccg ccc cag ata tcc atc ata ttc 158
 Lys Glu Leu Lys Tyr Ser Lys Asp Pro Pro Gln Ile Ser Ile Ile Phe
 15 20 25
 atc ttc gtg aac gag gcc ctg tcg gtg atc ctg cgg tcc gtg cac agt 206
 Ile Phe Val Asn Glu Ala Leu Ser Val Ile Leu Arg Ser Val His Ser
 30 35 40
 gcc gtc aat cac acg ccc aca cac ctg ctg aag gaa atc att ctg gtg 254
 Ala Val Asn His Thr Pro Thr His Leu Leu Lys Glu Ile Ile Leu Val

45	50	55	60	
gat gac aac agc gac gaa gag gag ctg aag gtc ccc cta gag gag tat	302			
Asp Asp Asn Ser Asp Glu Glu Glu Leu Lys Val Pro Leu Glu Glu Tyr				
65 70 75				
gtc cac aaa cgc tac ccc ggg ctg gtg aag gtg gta aga aat cag aag	350			
Val His Lys Arg Tyr Pro Gly Leu Val Lys Val Val Arg Asn Gln Lys				
80 85 90				
agg gaa ggc ctg atc cgc gct cgc att gag ggc tgg aag gtg gct acc	398			
Arg Glu Gly Leu Ile Arg Ala Arg Ile Glu Gly Trp Lys Val Ala Thr				
95 100 105				
ggg cag gtc act ggc ttc ttt gat gcc cac gtg gaa ttc acc gct ggc	446			
Gly Gln Val Thr Gly Phe Phe Asp Ala His Val Glu Phe Thr Ala Gly				
110 115 120				
tgg gct gag ccg gtt cta tcc cgc atc cag gaa aac cgg aag cgt gtg	494			
Trp Ala Glu Pro Val Leu Ser Arg Ile Gln Glu Asn Arg Lys Arg Val				
125 130 135 140				
atc ctc ccc tcc att gac aac atc aaa cag gac aac ttt gag gtg cag	542			
Ile Leu Pro Ser Ile Asp Asn Ile Lys Gln Asp Asn Phe Glu Val Gln				
145 150 155				
cgg tac gag aac tcg gcc cac ggg tac agc tgg gag ctg tgg tgc atg	590			
Arg Tyr Glu Asn Ser Ala His Gly Tyr Ser Trp Glu Leu Trp Cys Met				
160 165 170				
tac atc agc ccc cca aaa gac tgg tgg gac gcc gga gac cct tct ctc	638			
Tyr Ile Ser Pro Pro Lys Asp Trp Trp Asp Ala Gly Asp Pro Ser Leu				
175 180 185				
ccc atc agg acc cca gcc atg ata ggc tgc tcg ttc gtg gtc aac agg	686			
Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val Val Asn Arg				
190 195 200				
aag ttc ttc ggt gaa att ggt ctt ctg gat cct ggc atg gat gta tac	734			
Lys Phe Phe Gly Glu Ile Gly Leu Leu Asp Pro Gly Met Asp Val Tyr				
205 210 215 220				
gga gga gaa aat att gaa ctg gga atc aag gta tgg ctc tgt ggg ggc	782			
Gly Gly Glu Asn Ile Glu Leu Gly Ile Lys Val Trp Leu Cys Gly Gly				
225 230 235				
agc atg gag gtc ctt cct tgc tca cgg gtg gcc cac att gag cgg aag	830			
Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile Glu Arg Lys				
240 245 250				
aag aag cca tat aat agc aac att ggc ttc tac acc aag agg aat gct	878			
Lys Lys Pro Tyr Asn Ser Asn Ile Gly Phe Tyr Thr Lys Arg Asn Ala				
255 260 265				
ctt cgc gtt gct gag gtc tgg atg gac gat tac aag tct cat gtg tac	926			
Leu Arg Val Ala Glu Val Trp Met Asp Asp Tyr Lys Ser His Val Tyr				
270 275 280				

ata gcg tgg aac ctg ccg ctg gag aat ccg gga att gac atc ggt gat	974
Ile Ala Trp Asn Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly Asp	
285 290 295 300	
gtc tcc gaa aga aga gca tta agg aaa agt tta aag tgt aag aat ttc	1022
Val Ser Glu Arg Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn Phe	
305 310 315	
cag tgg tac ctg gac cat gtt tac cca gaa atg aga aga tac aat aat	1070
Gln Trp Tyr Leu Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn Asn	
320 325 330	
acc gtt gct tac ggg gag ctt cgc aac aac aag gca aaa gac gtc tgc	1118
Thr Val Ala Tyr Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val Cys	
335 340 345	
ttg gac cag ggg ccg ctg gag aac cac aca gca ata ttg tat ccg tgc	1166
Leu Asp Gln Gly Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro Cys	
350 355 360	
cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc ctg	1214
His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu	
365 370 375 380	
cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc tgc	1262
His Leu Gly Ala Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys	
385 390 395	
ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc gac	1310
Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp	
400 405 410	
aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat gga	1358
Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly	
415 420 425	
gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac cgg	1406
Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg	
430 435 440	
ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag agg	1454
Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg	
445 450 455 460	
tgg acc att aag aac tcc atc aag tagagggagg gagctggggc actggagcct	1508
Trp Thr Ile Lys Asn Ser Ile Lys	
465	
ggccccagg acatggctgc tcccccaac atctggacca gctgccctgg cggagagaca	1568
gcaaggggccc ggcaggtgct cgatggggccc cccagggctt ctccagggca gcacagggac	1628
cccggatgaa gactctgtcc cccctcaggc attcagctgc ccacaagttt cctgcaccct	1688
ggaaaagccc cccacccttc ctctgggaaa ctgacagctg tcttcacag cctctgatgt	1748

ggacctggta ctgaggagca agactgtcca gttctcctcc acatctccca tcccagaatc 1808
 aggatctggg actggcaggg tcccctcctg tgtctcatct cttgcagcag cagctgctga 1868
 actccagcca tcaacacggg gggaggcagc gggggcttca gccatgtcct agctccccgc 1928
 cctaaaagga ggcagtgagg accaggcact atttctcctg aggttacttc taccagatg 1988
 acacctgcct gttcacgccc caaggcagct actgccccta acccttccca ccagggtagc 2048
 tttgggcact gcagctctgg acttttctgg cccctcctga gatgacctga tggagctgat 2108
 gctttctctc ctaatccctg ggcactaggg tcttatcagt gtgcttgggc cagctctcct 2168
 gcctgtgtct agaggaagcc agagacagaa ataggctaag cctgcagtag gatctcagcc 2228
 acaagggccc cgcaggatgg agctgggtca aggaccaggg agccctgact cccagaggct 2288
 gccaccgggg agaagcagcg gtctccatc cagaacctaa gggctgaagc aaaggctgcc 2348
 aggacccttg aagatgcttt tggctcacct catttcaccc cacgctctgc tggctggcag 2408
 aggagaaggc agtcgtttcc tctctgaaga gtattttttt cgattgccct ctgggttaggg 2468
 tgcacatata aatcagagtt aatatatgaa cgcgtgtgca tgcacaagtg tgtgtgtgcc 2528
 tgcgtgctgt gcgtggcagg gtgtgtgtgt gtgtgtctgg ctgtgcgttc cggagtgtgt 2588
 gacgatgctg acctagctgt gtggccttgg gcttgctgct tcattactca cctggatggg 2648
 gacgagggat gagaaggggtg tgggtttggc cccatgtcac tggccggaag gatgtgtctc 2708
 agccctgccc tgtgggggtgc cccgatggg aggctgtccc atctcccagt ccccatctct 2768
 ttttccccac actgtccctg gccaaacct gccagagct gaacctgtga gctgccccct 2828
 tgccctgtgt gggattcgca gtgtctcatt tggtagcgtc ttactggtga tcctctctc 2888
 acccatctc ccaccttggt gaataaatac atgttagcac ttcccagagc agcctccttt 2948
 gtgtcttgat ttctccagaa ctggaggtgg ggaggggagt gatggagaca taggaggaga 3008
 gcttctttgg ctttgagggt ttagtgttac ttatttatct atttattcga gatggggctc 3068
 tgctctgtgg cccaggctgg agtgcagtgg tgcaatcatg a 3109

<210> 62

<211> 468

<212> PRT

<213> Homo sapiens

<400> 62

Met	Lys	Arg	Arg	Ser	Gly	Thr	Pro	Thr	Thr	Leu	Cys	Lys	Glu	Leu	Lys
1				5					10					15	

Tyr	Ser	Lys	Asp	Pro	Pro	Gln	Ile	Ser	Ile	Ile	Phe	Ile	Phe	Val	Asn
			20					25						30	

Glu	Ala	Leu	Ser	Val	Ile	Leu	Arg	Ser	Val	His	Ser	Ala	Val	Asn	His		
		35					40					45					
Thr	Pro	Thr	His	Leu	Leu	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Asn	Ser		
		50				55					60						
Asp	Glu	Glu	Glu	Leu	Lys	Val	Pro	Leu	Glu	Glu	Tyr	Val	His	Lys	Arg		
	65				70					75					80		
Tyr	Pro	Gly	Leu	Val	Lys	Val	Val	Arg	Asn	Gln	Lys	Arg	Glu	Gly	Leu		
			85						90					95			
Ile	Arg	Ala	Arg	Ile	Glu	Gly	Trp	Lys	Val	Ala	Thr	Gly	Gln	Val	Thr		
			100					105					110				
Gly	Phe	Phe	Asp	Ala	His	Val	Glu	Phe	Thr	Ala	Gly	Trp	Ala	Glu	Pro		
		115					120					125					
Val	Leu	Ser	Arg	Ile	Gln	Glu	Asn	Arg	Lys	Arg	Val	Ile	Leu	Pro	Ser		
	130					135					140						
Ile	Asp	Asn	Ile	Lys	Gln	Asp	Asn	Phe	Glu	Val	Gln	Arg	Tyr	Glu	Asn		
145					150					155					160		
Ser	Ala	His	Gly	Tyr	Ser	Trp	Glu	Leu	Trp	Cys	Met	Tyr	Ile	Ser	Pro		
			165					170						175			
Pro	Lys	Asp	Trp	Trp	Asp	Ala	Gly	Asp	Pro	Ser	Leu	Pro	Ile	Arg	Thr		
			180					185						190			
Pro	Ala	Met	Ile	Gly	Cys	Ser	Phe	Val	Val	Asn	Arg	Lys	Phe	Phe	Gly		
		195					200					205					
Glu	Ile	Gly	Leu	Leu	Asp	Pro	Gly	Met	Asp	Val	Tyr	Gly	Gly	Glu	Asn		
	210					215					220						
Ile	Glu	Leu	Gly	Ile	Lys	Val	Trp	Leu	Cys	Gly	Gly	Ser	Met	Glu	Val		
225					230					235					240		
Leu	Pro	Cys	Ser	Arg	Val	Ala	His	Ile	Glu	Arg	Lys	Lys	Lys	Pro	Tyr		
				245					250					255			
Asn	Ser	Asn	Ile	Gly	Phe	Tyr	Thr	Lys	Arg	Asn	Ala	Leu	Arg	Val	Ala		
			260					265					270				
Glu	Val	Trp	Met	Asp	Asp	Tyr	Lys	Ser	His	Val	Tyr	Ile	Ala	Trp	Asn		
		275					280					285					
Leu	Pro	Leu	Glu	Asn	Pro	Gly	Ile	Asp	Ile	Gly	Asp	Val	Ser	Glu	Arg		
	290					295					300						
Arg	Ala	Leu	Arg	Lys	Ser	Leu	Lys	Cys	Lys	Asn	Phe	Gln	Trp	Tyr	Leu		
305					310					315					320		
Asp	His	Val	Tyr	Pro	Glu	Met	Arg	Arg	Tyr	Asn	Asn	Thr	Val	Ala	Tyr		
				325					330					335			

Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val Cys Leu Asp Gln Gly
 340 345 350
 Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro Cys His Gly Trp Gly
 355 360 365
 Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu His Leu Gly Ala
 370 375 380
 Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys Leu Val Asp Asn
 385 390 395 400
 Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp Lys Val Lys Ser
 405 410 415
 Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly Ala Ile Met Asn
 420 425 430
 Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg Gly Leu Ala Gly
 435 440 445
 Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys
 450 455 460
 Asn Ser Ile Lys
 465

<210> 63
 <211> 1306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1306)

<400> 63
 c acc aga tct cgg tcc gtg cac agt gcc gtc aat cac acg ccc aca cac 49
 Thr Arg Ser Arg Ser Val His Ser Ala Val Asn His Thr Pro Thr His
 1 5 10 15
 ctg ctg aag gaa atc att ctg gtg gat gac aac agc gac gaa gag gag 97
 Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Asn Ser Asp Glu Glu Glu
 20 25 30
 ctg aag gtc ccc cta gag gag tat gtc cac aaa cgc tac ccc ggg ctg 145
 Leu Lys Val Pro Leu Glu Glu Tyr Val His Lys Arg Tyr Pro Gly Leu
 35 40 45
 gtg aag gtg gta aga aat cag aag agg gaa ggc ctg atc cgc gct cgc 193
 Val Lys Val Val Arg Asn Gln Lys Arg Glu Gly Leu Ile Arg Ala Arg
 50 55 60
 att gag ggc tgg aag gtg gct acc ggg cag gtc act ggc ttc ttt gat 241
 Ile Glu Gly Trp Lys Val Ala Thr Gly Gln Val Thr Gly Phe Phe Asp
 65 70 75 80

gcc cac gtg gaa ttc acc gct ggc tgg gct gag ccg gtt cta tcc cgc	289
Ala His Val Glu Phe Thr Ala Gly Trp Ala Glu Pro Val Leu Ser Arg	
85 90 95	
atc cag gaa aac cgg aag cgt gtg atc ctc ccc tcc att gac aac atc	337
Ile Gln Glu Asn Arg Lys Arg Val Ile Leu Pro Ser Ile Asp Asn Ile	
100 105 110	
aaa cag gac aac ttt gag gtg cag cgg tac gag aac tcg gcc cac ggg	385
Lys Gln Asp Asn Phe Glu Val Gln Arg Tyr Glu Asn Ser Ala His Gly	
115 120 125	
tac agc tgg gag ctg tgg tgc atg tac atc agc ccc cca aaa gac tgg	433
Tyr Ser Trp Glu Leu Trp Cys Met Tyr Ile Ser Pro Pro Lys Asp Trp	
130 135 140	
tgg gac gcc gga gac cct tct ctc ccc atc agg acc cca gcc atg ata	481
Trp Asp Ala Gly Asp Pro Ser Leu Pro Ile Arg Thr Pro Ala Met Ile	
145 150 155 160	
ggc tgc tcg ttc gtg gtc aac agg aag ttc ttc ggt gaa att ggt ctt	529
Gly Cys Ser Phe Val Val Asn Arg Lys Phe Phe Gly Glu Ile Gly Leu	
165 170 175	
ctg gat cct ggc atg gat gta tac gga gga gaa aat att gaa ctg gga	577
Leu Asp Pro Gly Met Asp Val Tyr Gly Gly Glu Asn Ile Glu Leu Gly	
180 185 190	
atc aag gta tgg ctc tgt ggg ggc agc atg gag gtc ctt cct tgc tca	625
Ile Lys Val Trp Leu Cys Gly Gly Ser Met Glu Val Leu Pro Cys Ser	
195 200 205	
cgg gtg gcc cac att gag cgg aag aag aag cca tat aat agc aac att	673
Arg Val Ala His Ile Glu Arg Lys Lys Lys Pro Tyr Asn Ser Asn Ile	
210 215 220	
ggc ttc tac acc aag agg aat gct ctt cgc gtt gct gag gtc tgg atg	721
Gly Phe Tyr Thr Lys Arg Asn Ala Leu Arg Val Ala Glu Val Trp Met	
225 230 235 240	
gac gat tac aag tct cat gtg tac ata gcg tgg aac ctg ccg ctg gag	769
Asp Asp Tyr Lys Ser His Val Tyr Ile Ala Trp Asn Leu Pro Leu Glu	
245 250 255	
aat ccg gga att gac atc ggt gat gtc tcc gaa aga aga gca tta agg	817
Asn Pro Gly Ile Asp Ile Gly Asp Val Ser Glu Arg Arg Ala Leu Arg	
260 265 270	
aaa agt tta aag tgt aag aat ttc cag tgg tac ctg gac cat gtt tac	865
Lys Ser Leu Lys Cys Lys Asn Phe Gln Trp Tyr Leu Asp His Val Tyr	
275 280 285	
cca gaa atg aga aga tac aat aat acc gtt gct tac ggg gag ctt cgc	913
Pro Glu Met Arg Arg Tyr Asn Asn Thr Val Ala Tyr Gly Glu Leu Arg	
290 295 300	

aac aac aag gca aaa gac gtc tgc ttg gac cag ggg ccg ctg gag aac	961
Asn Asn Lys Ala Lys Asp Val Cys Leu Asp Gln Gly Pro Leu Glu Asn	
305 310 315 320	
cac aca gca ata ttg tat ccg tgc cat ggc tgg gga cca cag ctt gcc	1009
His Thr Ala Ile Leu Tyr Pro Cys His Gly Trp Gly Pro Gln Leu Ala	
325 330 335	
cgc tac acc aag gaa ggc ttc ctg cac ttg ggt gcc ctg ggg acc acc	1057
Arg Tyr Thr Lys Glu Gly Phe Leu His Leu Gly Ala Leu Gly Thr Thr	
340 345 350	
aca ctc ctc cct gac acc cgc tgc ctg gtg gac aac tcc aag agt cgg	1105
Thr Leu Leu Pro Asp Thr Arg Cys Leu Val Asp Asn Ser Lys Ser Arg	
355 360 365	
ctg ccc cag ctc ctg gac tgc gac aag gtc aag agc agc ctg tac aag	1153
Leu Pro Gln Leu Leu Asp Cys Asp Lys Val Lys Ser Ser Leu Tyr Lys	
370 375 380	
cgc tgg aac ttc atc cag aat gga gcc atc atg aac aag ggc acg gga	1201
Arg Trp Asn Phe Ile Gln Asn Gly Ala Ile Met Asn Lys Gly Thr Gly	
385 390 395 400	
cgc tgc ctg gag gtg gag aac cgg ggc ctg gct ggc atc gac ctc atc	1249
Arg Cys Leu Glu Val Glu Asn Arg Gly Leu Ala Gly Ile Asp Leu Ile	
405 410 415	
ctc cgc agc tgc aca ggt cag agg tgg acc att aag aac tcc atc aag	1297
Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys Asn Ser Ile Lys	
420 425 430	
ctc gag ggc	1306
Leu Glu Gly	
435	
<210> 64	
<211> 435	
<212> PRT	
<213> Homo sapiens	
<400> 64	
Thr Arg Ser Arg Ser Val His Ser Ala Val Asn His Thr Pro Thr His	
1 5 10 15	
Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Asn Ser Asp Glu Glu Glu	
20 25 30	
Leu Lys Val Pro Leu Glu Glu Tyr Val His Lys Arg Tyr Pro Gly Leu	
35 40 45	
Val Lys Val Val Arg Asn Gln Lys Arg Glu Gly Leu Ile Arg Ala Arg	
50 55 60	
Ile Glu Gly Trp Lys Val Ala Thr Gly Gln Val Thr Gly Phe Phe Asp	
65 70 75 80	

Ala	His	Val	Glu	Phe	Thr	Ala	Gly	Trp	Ala	Glu	Pro	Val	Leu	Ser	Arg		
				85					90					95			
Ile	Gln	Glu	Asn	Arg	Lys	Arg	Val	Ile	Leu	Pro	Ser	Ile	Asp	Asn	Ile		
			100					105					110				
Lys	Gln	Asp	Asn	Phe	Glu	Val	Gln	Arg	Tyr	Glu	Asn	Ser	Ala	His	Gly		
		115					120					125					
Tyr	Ser	Trp	Glu	Leu	Trp	Cys	Met	Tyr	Ile	Ser	Pro	Pro	Lys	Asp	Trp		
	130					135					140						
Trp	Asp	Ala	Gly	Asp	Pro	Ser	Leu	Pro	Ile	Arg	Thr	Pro	Ala	Met	Ile		
145					150					155					160		
Gly	Cys	Ser	Phe	Val	Val	Asn	Arg	Lys	Phe	Phe	Gly	Glu	Ile	Gly	Leu		
				165					170					175			
Leu	Asp	Pro	Gly	Met	Asp	Val	Tyr	Gly	Gly	Glu	Asn	Ile	Glu	Leu	Gly		
			180					185					190				
Ile	Lys	Val	Trp	Leu	Cys	Gly	Gly	Ser	Met	Glu	Val	Leu	Pro	Cys	Ser		
		195					200					205					
Arg	Val	Ala	His	Ile	Glu	Arg	Lys	Lys	Lys	Pro	Tyr	Asn	Ser	Asn	Ile		
	210					215						220					
Gly	Phe	Tyr	Thr	Lys	Arg	Asn	Ala	Leu	Arg	Val	Ala	Glu	Val	Trp	Met		
225					230					235					240		
Asp	Asp	Tyr	Lys	Ser	His	Val	Tyr	Ile	Ala	Trp	Asn	Leu	Pro	Leu	Glu		
				245					250					255			
Asn	Pro	Gly	Ile	Asp	Ile	Gly	Asp	Val	Ser	Glu	Arg	Arg	Ala	Leu	Arg		
			260					265					270				
Lys	Ser	Leu	Lys	Cys	Lys	Asn	Phe	Gln	Trp	Tyr	Leu	Asp	His	Val	Tyr		
		275					280					285					
Pro	Glu	Met	Arg	Arg	Tyr	Asn	Asn	Thr	Val	Ala	Tyr	Gly	Glu	Leu	Arg		
	290					295					300						
Asn	Asn	Lys	Ala	Lys	Asp	Val	Cys	Leu	Asp	Gln	Gly	Pro	Leu	Glu	Asn		
305					310					315				320			
His	Thr	Ala	Ile	Leu	Tyr	Pro	Cys	His	Gly	Trp	Gly	Pro	Gln	Leu	Ala		
				325					330					335			
Arg	Tyr	Thr	Lys	Glu	Gly	Phe	Leu	His	Leu	Gly	Ala	Leu	Gly	Thr	Thr		
			340					345					350				
Thr	Leu	Leu	Pro	Asp	Thr	Arg	Cys	Leu	Val	Asp	Asn	Ser	Lys	Ser	Arg		
		355					360					365					
Leu	Pro	Gln	Leu	Leu	Asp	Cys	Asp	Lys	Val	Lys	Ser	Ser	Leu	Tyr	Lys		
	370					375					380						

Arg Trp Asn Phe Ile Gln Asn Gly Ala Ile Met Asn Lys Gly Thr Gly
385 390 395 400

Arg Cys Leu Glu Val Glu Asn Arg Gly Leu Ala Gly Ile Asp Leu Ile
405 410 415

Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys Asn Ser Ile Lys
420 425 430

Leu Glu Gly
435

<210> 65

<211> 3109

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)..(1478)

<400> 65

aggggctgag gaggtactgg aaaagaaaga ggagcaggag ctggaggaag acgtggagga 60

ggagctggag gagg atg aag aga agg agt ggg acg ccc aca acc ctg tgt 110
Met Lys Arg Arg Ser Gly Thr Pro Thr Thr Leu Cys
1 5 10

aag gag ctc aag tac tcc aag gac ccg ccc cag ata tcc atc ata ttc 158
Lys Glu Leu Lys Tyr Ser Lys Asp Pro Pro Gln Ile Ser Ile Ile Phe
15 20 25

atc ttc gtg aac gag gcc ctg tcg gtg atc ctg cgg tcc gtg cac agt 206
Ile Phe Val Asn Glu Ala Leu Ser Val Ile Leu Arg Ser Val His Ser
30 35 40

gcc gtc aat cac acg ccc aca cac ctg ctg aag gaa atc att ctg gtg 254
Ala Val Asn His Thr Pro Thr His Leu Leu Lys Glu Ile Ile Leu Val
45 50 55 60

gat gac aac agc gac gaa gag gag ctg aag gtc ccc cta gag gag tat 302
Asp Asp Asn Ser Asp Glu Glu Glu Leu Lys Val Pro Leu Glu Glu Tyr
65 70 75

gtc cac aaa cgc tac ccc ggg ctg gtg aag gtg gta aga aat cag aag 350
Val His Lys Arg Tyr Pro Gly Leu Val Lys Val Val Arg Asn Gln Lys
80 85 90

agg gaa ggc ctg atc cgc gct cgc att gag ggc tgg aag gtg gct acc 398
Arg Glu Gly Leu Ile Arg Ala Arg Ile Glu Gly Trp Lys Val Ala Thr
95 100 105

ggg cag gtc act ggc ttc ttt gat gcc cac gtg gaa ttc acc gct ggc 446
Gly Gln Val Thr Gly Phe Phe Asp Ala His Val Glu Phe Thr Ala Gly
110 115 120

tgg gct gag ccg gtt cta tcc cgc atc cag gaa aac cgg aag cgt gtg 494

Trp	Ala	Glu	Pro	Val	Leu	Ser	Arg	Ile	Gln	Glu	Asn	Arg	Lys	Arg	Val		
125					130					135					140		
atc	ctc	ccc	tcc	att	gac	aac	atc	aaa	cag	gac	aac	ttt	gag	gtg	cag	542	
Ile	Leu	Pro	Ser	Ile	Asp	Asn	Ile	Lys	Gln	Asp	Asn	Phe	Glu	Val	Gln		
				145					150					155			
cgg	tac	gag	aac	tcg	gcc	cac	ggg	tac	ggc	tgg	gag	ctg	tgg	tgc	atg	590	
Arg	Tyr	Glu	Asn	Ser	Ala	His	Gly	Tyr	Gly	Trp	Glu	Leu	Trp	Cys	Met		
			160					165					170				
tac	atc	agc	ccc	cca	aaa	gac	tgg	tgg	gac	gcc	gga	gac	cct	tct	ctc	638	
Tyr	Ile	Ser	Pro	Pro	Lys	Asp	Trp	Trp	Asp	Ala	Gly	Asp	Pro	Ser	Leu		
		175					180					185					
ccc	atc	agg	acc	cca	gcc	atg	ata	ggc	tgc	tcg	ttc	gtg	gtc	aac	agg	686	
Pro	Ile	Arg	Thr	Pro	Ala	Met	Ile	Gly	Cys	Ser	Phe	Val	Val	Asn	Arg		
	190					195					200						
aag	ttc	ttc	ggg	gaa	att	ggg	ctt	ctg	gat	cct	ggc	atg	gat	gta	tac	734	
Lys	Phe	Phe	Gly	Glu	Ile	Gly	Leu	Leu	Asp	Pro	Gly	Met	Asp	Val	Tyr		
205					210					215					220		
gga	gga	gaa	aat	att	gaa	ctg	gga	atc	aag	gta	tgg	ctc	tgt	ggg	ggc	782	
Gly	Gly	Glu	Asn	Ile	Glu	Leu	Gly	Ile	Lys	Val	Trp	Leu	Cys	Gly	Gly		
			225					230					235				
agc	atg	gag	gtc	ctt	cct	tgc	tca	cgg	gtg	gcc	cac	att	gag	cgg	aag	830	
Ser	Met	Glu	Val	Leu	Pro	Cys	Ser	Arg	Val	Ala	His	Ile	Glu	Arg	Lys		
			240					245					250				
aag	aag	cca	tat	aat	agc	aac	att	ggc	ttc	tac	acc	aag	agg	aat	gct	878	
Lys	Lys	Pro	Tyr	Asn	Ser	Asn	Ile	Gly	Phe	Tyr	Thr	Lys	Arg	Asn	Ala		
		255					260					265					
ctt	cgc	gtt	gct	gag	gtc	tgg	atg	gac	gat	tac	aag	tct	cat	gtg	tac	926	
Leu	Arg	Val	Ala	Glu	Val	Trp	Met	Asp	Asp	Tyr	Lys	Ser	His	Val	Tyr		
	270					275					280						
ata	gcg	tgg	aac	ctg	ccg	ctg	gag	aat	ccg	gga	att	gac	atc	ggg	gat	974	
Ile	Ala	Trp	Asn	Leu	Pro	Leu	Glu	Asn	Pro	Gly	Ile	Asp	Ile	Gly	Asp		
285					290				295					300			
gtc	tcc	gaa	aga	aga	gca	tta	agg	aaa	agt	tta	aag	tgt	aag	aat	ttc	1022	
Val	Ser	Glu	Arg	Arg	Ala	Leu	Arg	Lys	Ser	Leu	Lys	Cys	Lys	Asn	Phe		
				305				310						315			
cag	tgg	tac	ctg	gac	cat	gtt	tac	cca	gaa	atg	aga	aga	tac	aat	aat	1070	
Gln	Trp	Tyr	Leu	Asp	His	Val	Tyr	Pro	Glu	Met	Arg	Arg	Tyr	Asn	Asn		
			320					325					330				
acc	gtt	gct	tac	ggg	gag	ctt	cgc	aac	aac	aag	gca	aaa	gac	gtc	tgc	1118	
Thr	Val	Ala	Tyr	Gly	Glu	Leu	Arg	Asn	Asn	Lys	Ala	Lys	Asp	Val	Cys		
		335					340					345					
ttg	gac	cag	ggg	ccg	ctg	gag	aac	cac	aca	gca	ata	ttg	tat	ccg	tgc	1166	
Leu	Asp	Gln	Gly	Pro	Leu	Glu	Asn	His	Thr	Ala	Ile	Leu	Tyr	Pro	Cys		

350	355	360	
cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc ctg			1214
His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu			
365	370	375	380
cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc tgc			1262
His Leu Gly Ala Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys			
	385	390	395
ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc gac			1310
Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp			
	400	405	410
aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat gga			1358
Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly			
	415	420	425
gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac cgg			1406
Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg			
	430	435	440
ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag agg			1454
Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg			
	445	450	455
tgg acc att aag aac tcc atc aag tagagggagg gagctggggc actggagcct			1508
Trp Thr Ile Lys Asn Ser Ile Lys			
	465		
ggcccccagg acatggctgc tcccccaac atctggacca gctgccttgg cggagagaca			1568
gcaagggggcc ggcaggtgct cgatggggccc cccagggctt ctccagggca gcacagggac			1628
cccggatgaa gactctgtcc cccctcaggc attcagctgc ccacaagttt cctgcaccct			1688
ggaaaagccc cccacccttc ctctgggaaa ctgacagctg tcttcacag cctctgatgt			1748
ggacctggta ctgaggagca agactgtcca gttctcctcc acatctccca tcccagaatc			1808
aggatctggg actggcaggg tcccctcctg tgtctcatct cttgcagcag cagctgctga			1868
actccagcca tcaacacggt gggaggcagc gggggcttca gccatgtcct agctccccgc			1928
cctaaaagga ggcagtgagg accaggcact atttcctccg aggttacttc taccagatg			1988
acacctgcct gttcacgccc caaggcagct actgccccta acccttccca ccagggtagc			2048
tttgggcact gcagctctgg acttttctgg cccctcctga gatgacctga tggagctgat			2108
gctttctctc ctaatccctg ggcactaggc tcttatcagt gtgcttgggc cagctctcct			2168
gcctgtgtct agaggaagcc agagacagaa ataggctaag cctgcagtag gatctcagcc			2228
acaagggccc cgcaggatgg agctgggtca aggaccaggg agccctgact cccagaggct			2288
gccaccgggg agaagcagcg gtcctccatc cagaacctaa gggctgaagc aaaggctgcc			2348

aggacccttg aagatgcttt tggctcacct catttcaccc cacgctctgc tggctggcag 2408
 aggagaaggc agtcgtttcc tctctgaaga gtattttttt cgattgccct ctgggttaggg 2468
 tgcacatata aatcagagtt aatatatgaa cgcgtgtgca tgcacaagtg tgtgtgtgcc 2528
 tgcgtgctgt gcgtggcagg gtgtgtgtgt gtgtgtctgg ctgtgcgttc cggagtgtgt 2588
 gacgatgctg acctagctgt gtggccttgg gcttgcctgt tcattactca cctggatggg 2648
 gacgagggat gagaaggggtg tgggtttggc cccatgtcac tggccggaag gatgtgtctc 2708
 agccctgccc tgtgggggtgc cccgatggg aggetgtccc atctcccagt ccccatctct 2768
 ttttccccac actgtccctg gccagccct gccagagct gaacctgtga gctgccccct 2828
 tgccctgtgt gggattcgca gtgtctcatt tggtgacgtc ttactgggtga tcatctcctc 2888
 acccatctc ccaccttgtg gaataaatac atgttagcac ttcccagagc agcctccttt 2948
 gtgtcttgat ttctccagaa ctggaggtgg ggaggggagt gatggagaca taggaggaga 3008
 gcttctttgg ctttgagggt ttagtgttac ttatttatct atttattcga gatgggggtct 3068
 tgctctgtgg ccaggtctgg agtgcagtgg tgcaatcatg a 3109

<210> 66

<211> 468

<212> PRT

<213> Homo sapiens

<400> 66

Met	Lys	Arg	Arg	Ser	Gly	Thr	Pro	Thr	Thr	Leu	Cys	Lys	Glu	Leu	Lys
1				5					10					15	
Tyr	Ser	Lys	Asp	Pro	Pro	Gln	Ile	Ser	Ile	Ile	Phe	Ile	Phe	Val	Asn
			20					25						30	
Glu	Ala	Leu	Ser	Val	Ile	Leu	Arg	Ser	Val	His	Ser	Ala	Val	Asn	His
		35					40					45			
Thr	Pro	Thr	His	Leu	Leu	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Asn	Ser
		50				55					60				
Asp	Glu	Glu	Glu	Leu	Lys	Val	Pro	Leu	Glu	Glu	Tyr	Val	His	Lys	Arg
65					70					75				80	
Tyr	Pro	Gly	Leu	Val	Lys	Val	Val	Arg	Asn	Gln	Lys	Arg	Glu	Gly	Leu
			85						90					95	
Ile	Arg	Ala	Arg	Ile	Glu	Gly	Trp	Lys	Val	Ala	Thr	Gly	Gln	Val	Thr
			100					105					110		
Gly	Phe	Phe	Asp	Ala	His	Val	Glu	Phe	Thr	Ala	Gly	Trp	Ala	Glu	Pro
		115					120					125			

Val	Leu	Ser	Arg	Ile	Gln	Glu	Asn	Arg	Lys	Arg	Val	Ile	Leu	Pro	Ser		
130						135					140						
Ile	Asp	Asn	Ile	Lys	Gln	Asp	Asn	Phe	Glu	Val	Gln	Arg	Tyr	Glu	Asn		
145					150					155					160		
Ser	Ala	His	Gly	Tyr	Gly	Trp	Glu	Leu	Trp	Cys	Met	Tyr	Ile	Ser	Pro		
			165						170					175			
Pro	Lys	Asp	Trp	Trp	Asp	Ala	Gly	Asp	Pro	Ser	Leu	Pro	Ile	Arg	Thr		
			180					185						190			
Pro	Ala	Met	Ile	Gly	Cys	Ser	Phe	Val	Val	Asn	Arg	Lys	Phe	Phe	Gly		
		195					200					205					
Glu	Ile	Gly	Leu	Leu	Asp	Pro	Gly	Met	Asp	Val	Tyr	Gly	Gly	Glu	Asn		
	210					215					220						
Ile	Glu	Leu	Gly	Ile	Lys	Val	Trp	Leu	Cys	Gly	Gly	Ser	Met	Glu	Val		
225					230					235					240		
Leu	Pro	Cys	Ser	Arg	Val	Ala	His	Ile	Glu	Arg	Lys	Lys	Lys	Pro	Tyr		
				245					250					255			
Asn	Ser	Asn	Ile	Gly	Phe	Tyr	Thr	Lys	Arg	Asn	Ala	Leu	Arg	Val	Ala		
			260					265					270				
Glu	Val	Trp	Met	Asp	Asp	Tyr	Lys	Ser	His	Val	Tyr	Ile	Ala	Trp	Asn		
	275						280					285					
Leu	Pro	Leu	Glu	Asn	Pro	Gly	Ile	Asp	Ile	Gly	Asp	Val	Ser	Glu	Arg		
	290					295					300						
Arg	Ala	Leu	Arg	Lys	Ser	Leu	Lys	Cys	Lys	Asn	Phe	Gln	Trp	Tyr	Leu		
305					310					315					320		
Asp	His	Val	Tyr	Pro	Glu	Met	Arg	Arg	Tyr	Asn	Asn	Thr	Val	Ala	Tyr		
				325					330					335			
Gly	Glu	Leu	Arg	Asn	Asn	Lys	Ala	Lys	Asp	Val	Cys	Leu	Asp	Gln	Gly		
		340						345					350				
Pro	Leu	Glu	Asn	His	Thr	Ala	Ile	Leu	Tyr	Pro	Cys	His	Gly	Trp	Gly		
		355					360					365					
Pro	Gln	Leu	Ala	Arg	Tyr	Thr	Lys	Glu	Gly	Phe	Leu	His	Leu	Gly	Ala		
	370					375					380						
Leu	Gly	Thr	Thr	Thr	Leu	Leu	Pro	Asp	Thr	Arg	Cys	Leu	Val	Asp	Asn		
385					390					395					400		
Ser	Lys	Ser	Arg	Leu	Pro	Gln	Leu	Leu	Asp	Cys	Asp	Lys	Val	Lys	Ser		
				405					410					415			
Ser	Leu	Tyr	Lys	Arg	Trp	Asn	Phe	Ile	Gln	Asn	Gly	Ala	Ile	Met	Asn		
			420				425						430				

Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg Gly Leu Ala Gly
435 440 445

Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys
450 455 460

Asn Ser Ile Lys
465

<210> 67

<211> 3109

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)..(1478)

<400> 67

aggggctgag gaggtactgg aaaagaaaga ggagcaggag ctggaggaag acgtggagga 60

ggagctggag gagg atg aag aga agg agt ggg acg ccc aca acc ctg tgt 110
Met Lys Arg Arg Ser Gly Thr Pro Thr Thr Leu Cys
1 5 10

aag gag ctc aag tac tcc aag gac ccg ccc cag ata tcc atc ata ttc 158
Lys Glu Leu Lys Tyr Ser Lys Asp Pro Pro Gln Ile Ser Ile Ile Phe
15 20 25

atc ttc gtg aac gag gcc ctg tcg gtg atc ctg cgg tcc gtg cac agt 206
Ile Phe Val Asn Glu Ala Leu Ser Val Ile Leu Arg Ser Val His Ser
30 35 40

gcc gtc aat cac acg ccc aca cac ctg ctg aag gaa atc att ctg gtg 254
Ala Val Asn His Thr Pro Thr His Leu Leu Lys Glu Ile Ile Leu Val
45 50 55 60

gat gac aac agc gac gaa gag gag ctg aag gtc ccc cta gag gag tat 302
Asp Asp Asn Ser Asp Glu Glu Glu Leu Lys Val Pro Leu Glu Glu Tyr
65 70 75

gtc cac aaa cgc tac ccc ggg ctg gtg aag gtg gta aga aat cag aag 350
Val His Lys Arg Tyr Pro Gly Leu Val Lys Val Val Arg Asn Gln Lys
80 85 90

agg gaa ggc ctg atc cgc gct cgc att gag ggc tgg aag gtg gct acc 398
Arg Glu Gly Leu Ile Arg Ala Arg Ile Glu Gly Trp Lys Val Ala Thr
95 100 105

ggg cag gtc act ggc ttc ttt gat gcc cac gtg gaa ttc acc gct ggc 446
Gly Gln Val Thr Gly Phe Phe Asp Ala His Val Glu Phe Thr Ala Gly
110 115 120

tgg gct gag ccg gtt cta tcc cgc atc cag gaa aac cgg aag cgt gtg 494
Trp Ala Glu Pro Val Leu Ser Arg Ile Gln Glu Asn Arg Lys Arg Val
125 130 135 140

atc ctc ccc tcc att gac aac atc aaa cag gac aac ttt gag gtg cag	542
Ile Leu Pro Ser Ile Asp Asn Ile Lys Gln Asp Asn Phe Glu Val Gln	
145 150 155	
cgg tac gag aac tcg gcc cac ggg tac agc tgg gag ctg tgg tgc atg	590
Arg Tyr Glu Asn Ser Ala His Gly Tyr Ser Trp Glu Leu Trp Cys Met	
160 165 170	
tac atc agc ccc cca aaa gac tgg tgg gac gcc gga gac cct tct ctc	638
Tyr Ile Ser Pro Pro Lys Asp Trp Trp Asp Ala Gly Asp Pro Ser Leu	
175 180 185	
ccc atc agg acc cca gcc atg ata ggc tgc tcg ttc gtg gtc aac agg	686
Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val Val Asn Arg	
190 195 200	
aag ttc ttc ggt gaa att ggt ctt ctg gat cct ggc atg gat gta tac	734
Lys Phe Phe Gly Glu Ile Gly Leu Leu Asp Pro Gly Met Asp Val Tyr	
205 210 215 220	
gga gga gaa aat att gaa ctg gga atc aag gta tgg ctc tgt ggg ggc	782
Gly Gly Glu Asn Ile Glu Leu Gly Ile Lys Val Trp Leu Cys Gly Gly	
225 230 235	
agc atg gag gtc ctt cct tgc tca cgg gtg gcc cac att gag cgg aag	830
Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile Glu Arg Lys	
240 245 250	
aag aag cca tat aat agc aac att ggc ttc tac acc aag agg aat gct	878
Lys Lys Pro Tyr Asn Ser Asn Ile Gly Phe Tyr Thr Lys Arg Asn Ala	
255 260 265	
ctt cgc gtt gct gag gtc tgg atg gac gat tac aag tct cat gtg tac	926
Leu Arg Val Ala Glu Val Trp Met Asp Asp Tyr Lys Ser His Val Tyr	
270 275 280	
ata gcg tgg aac ctg ccg ctg gag aat ccg gga att gac atc ggt gat	974
Ile Ala Trp Asn Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly Asp	
285 290 295 300	
gtc tcc gaa aga aga gca tta agg aaa agt tta aag tgt aag aat ttc	1022
Val Ser Glu Arg Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn Phe	
305 310 315	
cag tgg tac ctg gac cat gtt tac cca gaa atg aga aga tac aat aat	1070
Gln Trp Tyr Leu Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn Asn	
320 325 330	
acc gtt gct tac ggg gag ctt cgc aac aac aag gca aaa gac gtc tgc	1118
Thr Val Ala Tyr Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val Cys	
335 340 345	
ttg gac cag ggg ccg ctg gag aac cac aca gca ata ttg tat ccg tgc	1166
Leu Asp Gln Gly Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro Cys	
350 355 360	
cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc ctg	1214

His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu	
365	370 375 380
cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc tgc	1262
His Leu Gly Ala Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys	
	385 390 395
ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc gac	1310
Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp	
	400 405 410
aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat gga	1358
Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly	
	415 420 425
gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac cgg	1406
Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg	
	430 435 440
ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag agg	1454
Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg	
	445 450 455 460
tgg acc att aag aac tcc atc aag tagagggagg gagctggggc actggagcct	1508
Trp Thr Ile Lys Asn Ser Ile Lys	
	465
ggccccagg acatggctcc tcccccaac atctggacca gctgccttg cggagagaca	1568
gcaagggggcc ggcaggtgct cgatggggccc ccaggggctt ctccagggca gcacagggac	1628
cccggatgaa gactctgtcc cccctcaggc attcagctgc ccacaagttt cctgcaccct	1688
ggaaaagccc ccacccttc ctctgggaaa ctgacagctg tcttcacag cctctgatgt	1748
ggacctggta ctgaggagca agactgtcca gttctcctcc acatctccca tcccagaatc	1808
aggatctggg actggcaggg tcccctcctg tgtctcatct cttgcagcag cagctgctga	1868
actccagcca tcaacacggt gggaggcagc gggggcttca gccatgtcct agctccccgc	1928
cctaaaagga ggcagtgagg accaggcact atttctccg aggttacttc taccagatg	1988
acacctgcct gttcacgccc caaggcagct actgccccta acccttccca ccagggtagc	2048
tttgggcact gcagctctgg acttttctgg cccctcctga gatgacctga tggagctgat	2108
gctttctctc ctaatccctg ggcactagge tcttatcagt gtgcttgggc cagctctcct	2168
gcctgtgtct agaggaagcc agagacagaa ataggctaag cctgcagtag gatctcagcc	2228
acaagggccc cgcaggatgg agctgggtca aggaccaggg agccctgact ccagaggct	2288
gccaccgggg agaagcagcg gtcctccatc cagaacctaa gggctgaagc aaaggctgcc	2348
aggacccttg aagatgcttt tggtcacct catttcaccc cagctctgc tggctggcag	2408

aggagaaggc agtcgtttcc tctctgaaga gtatTTTTTTT cgattgccct ctggttaggg 2468
 tgcacatata aatcagagtt aatatatgaa cgcgtgtgca tgcacaagtg tgtgtgtgcc 2528
 tgcgtgctgt gcgtggcagg gtgtgtgtgt gtgtgtctgg ctgtgcgttc cggagtgtgt 2588
 gacgatgctg acctagctgt gtggccttgg gcttgcctgt tcattactca cctggatggg 2648
 gacgagggat gagaaggggtg tgggtttggc cccatgtcac tggccggaag gatgtgtctc 2708
 agccctgccc tgtgggggtgc ccccgatggg aggctgtccc atctcccagt ccccatctct 2768
 ttttccccac actgtccctg gccaaacct gccagagct gaacctgta gctgccccct 2828
 tgccctgtgt gggattcgca gtgtctcatt tgggtgacgtc ttactggtga tcattctctc 2888
 acccatctc ccacctgtg gaataaatac atgttagcac ttcccagagc agcctccttt 2948
 gtgtcttgat ttctccagaa ctggaggtgg ggaggggagt gatggagaca taggaggaga 3008
 gcttctttgg ctttgagggg ttagtggttac ttatttatct atttattcga gatgggggtct 3068
 tgctctgtgg ccaggtctgg agtgcagtgg tgcaatcatg a 3109

<210> 68

<211> 468

<212> PRT

<213> Homo sapiens

<400> 68

Met	Lys	Arg	Arg	Ser	Gly	Thr	Pro	Thr	Thr	Leu	Cys	Lys	Glu	Leu	Lys
1				5					10					15	
Tyr	Ser	Lys	Asp	Pro	Pro	Gln	Ile	Ser	Ile	Ile	Phe	Ile	Phe	Val	Asn
			20					25					30		
Glu	Ala	Leu	Ser	Val	Ile	Leu	Arg	Ser	Val	His	Ser	Ala	Val	Asn	His
		35					40					45			
Thr	Pro	Thr	His	Leu	Leu	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Asn	Ser
		50				55					60				
Asp	Glu	Glu	Glu	Leu	Lys	Val	Pro	Leu	Glu	Glu	Tyr	Val	His	Lys	Arg
65					70					75				80	
Tyr	Pro	Gly	Leu	Val	Lys	Val	Val	Arg	Asn	Gln	Lys	Arg	Glu	Gly	Leu
			85						90					95	
Ile	Arg	Ala	Arg	Ile	Glu	Gly	Trp	Lys	Val	Ala	Thr	Gly	Gln	Val	Thr
		100						105					110		
Gly	Phe	Phe	Asp	Ala	His	Val	Glu	Phe	Thr	Ala	Gly	Trp	Ala	Glu	Pro
		115					120				125				
Val	Leu	Ser	Arg	Ile	Gln	Glu	Asn	Arg	Lys	Arg	Val	Ile	Leu	Pro	Ser
	130					135					140				

Ile	Asp	Asn	Ile	Lys	Gln	Asp	Asn	Phe	Glu	Val	Gln	Arg	Tyr	Glu	Asn	145	150	155	160
Ser	Ala	His	Gly	Tyr	Ser	Trp	Glu	Leu	Trp	Cys	Met	Tyr	Ile	Ser	Pro	165	170	175	
Pro	Lys	Asp	Trp	Trp	Asp	Ala	Gly	Asp	Pro	Ser	Leu	Pro	Ile	Arg	Thr	180	185	190	
Pro	Ala	Met	Ile	Gly	Cys	Ser	Phe	Val	Val	Asn	Arg	Lys	Phe	Phe	Gly	195	200	205	
Glu	Ile	Gly	Leu	Leu	Asp	Pro	Gly	Met	Asp	Val	Tyr	Gly	Gly	Glu	Asn	210	215	220	
Ile	Glu	Leu	Gly	Ile	Lys	Val	Trp	Leu	Cys	Gly	Gly	Ser	Met	Glu	Val	225	230	235	240
Leu	Pro	Cys	Ser	Arg	Val	Ala	His	Ile	Glu	Arg	Lys	Lys	Lys	Pro	Tyr	245	250	255	
Asn	Ser	Asn	Ile	Gly	Phe	Tyr	Thr	Lys	Arg	Asn	Ala	Leu	Arg	Val	Ala	260	265	270	
Glu	Val	Trp	Met	Asp	Asp	Tyr	Lys	Ser	His	Val	Tyr	Ile	Ala	Trp	Asn	275	280	285	
Leu	Pro	Leu	Glu	Asn	Pro	Gly	Ile	Asp	Ile	Gly	Asp	Val	Ser	Glu	Arg	290	295	300	
Arg	Ala	Leu	Arg	Lys	Ser	Leu	Lys	Cys	Lys	Asn	Phe	Gln	Trp	Tyr	Leu	305	310	315	320
Asp	His	Val	Tyr	Pro	Glu	Met	Arg	Arg	Tyr	Asn	Asn	Thr	Val	Ala	Tyr	325	330	335	
Gly	Glu	Leu	Arg	Asn	Asn	Lys	Ala	Lys	Asp	Val	Cys	Leu	Asp	Gln	Gly	340	345	350	
Pro	Leu	Glu	Asn	His	Thr	Ala	Ile	Leu	Tyr	Pro	Cys	His	Gly	Trp	Gly	355	360	365	
Pro	Gln	Leu	Ala	Arg	Tyr	Thr	Lys	Glu	Gly	Phe	Leu	His	Leu	Gly	Ala	370	375	380	
Leu	Gly	Thr	Thr	Thr	Leu	Leu	Pro	Asp	Thr	Arg	Cys	Leu	Val	Asp	Asn	385	390	395	400
Ser	Lys	Ser	Arg	Leu	Pro	Gln	Leu	Leu	Asp	Cys	Asp	Lys	Val	Lys	Ser	405	410	415	
Ser	Leu	Tyr	Lys	Arg	Trp	Asn	Phe	Ile	Gln	Asn	Gly	Ala	Ile	Met	Asn	420	425	430	
Lys	Gly	Thr	Gly	Arg	Cys	Leu	Glu	Val	Glu	Asn	Arg	Gly	Leu	Ala	Gly	435	440	445	

Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys
 450 455 460

Asn Ser Ile Lys
 465

<210> 69
 <211> 3109
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(1478)

<400> 69
 aggggctgag gaggtactgg aaaagaaaga ggagcaggag ctggaggaag acgtggagga 60

ggagctggag gagg atg aag aga agg agt ggg acg ccc aca acc ctg tgt 110
 Met Lys Arg Arg Ser Gly Thr Pro Thr Thr Leu Cys
 1 5 10

aag gag ctc aag tac tcc aag gac ccg ccc cag ata tcc atc ata ttc 158
 Lys Glu Leu Lys Tyr Ser Lys Asp Pro Pro Gln Ile Ser Ile Ile Phe
 15 20 25

atc ttc gtg aac gag gcc ctg tcg gtg atc ctg cgg tcc gtg cac agt 206
 Ile Phe Val Asn Glu Ala Leu Ser Val Ile Leu Arg Ser Val His Ser
 30 35 40

gcc gtc aat cac acg ccc aca cac ctg ctg aag gaa atc att ctg gtg 254
 Ala Val Asn His Thr Pro Thr His Leu Leu Lys Glu Ile Ile Leu Val
 45 50 55 60

gat gac aac agc gac gaa gag gag ctg aag gtc ccc cta gag gag tat 302
 Asp Asp Asn Ser Asp Glu Glu Glu Leu Lys Val Pro Leu Glu Glu Tyr
 65 70 75

gtc cac aaa cgc tac ccc ggg ctg gtg aag gtg gta aga aat cag aag 350
 Val His Lys Arg Tyr Pro Gly Leu Val Lys Val Val Arg Asn Gln Lys
 80 85 90

agg gaa ggc ctg atc cgc gct cgc att gag ggc tgg aag gtg gct acc 398
 Arg Glu Gly Leu Ile Arg Ala Arg Ile Glu Gly Trp Lys Val Ala Thr
 95 100 105

ggg cag gtc act ggc ttc ttt gat gcc cac gtg gaa ttc acc gct ggc 446
 Gly Gln Val Thr Gly Phe Phe Asp Ala His Val Glu Phe Thr Ala Gly
 110 115 120

tgg gct gag ccg gtt cta tcc cgc atc cag gaa aac cgg aag cgt gtg 494
 Trp Ala Glu Pro Val Leu Ser Arg Ile Gln Glu Asn Arg Lys Arg Val
 125 130 135 140

atc ctc ccc tcc att gac aac atc aaa cag gac aac ttt gag gtg cag 542
 Ile Leu Pro Ser Ile Asp Asn Ile Lys Gln Asp Asn Phe Glu Val Gln
 145 150 155

cgg tac gag aac tcg gcc cac ggg tac agc tgg gag ctg tgg tgc atg	590
Arg Tyr Glu Asn Ser Ala His Gly Tyr Ser Trp Glu Leu Trp Cys Met	
160 165 170	
tac atc agc ccc cca aaa gac tgg tgg gac gcc gga gac cct tct ctc	638
Tyr Ile Ser Pro Pro Lys Asp Trp Trp Asp Ala Gly Asp Pro Ser Leu	
175 180 185	
ccc atc agg acc cca gcc atg ata ggc tgc tcg ttc gtg gtc aac agg	686
Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val Val Asn Arg	
190 195 200	
aag ttc ttc ggt gaa att ggt ctt ctg gat cct ggc atg gat gta tac	734
Lys Phe Phe Gly Glu Ile Gly Leu Leu Asp Pro Gly Met Asp Val Tyr	
205 210 215 220	
gga gga gaa aat att gaa ctg gga atc aag gta tgg ctc tgt ggg ggc	782
Gly Gly Glu Asn Ile Glu Leu Gly Ile Lys Val Trp Leu Cys Gly Gly	
225 230 235	
agc atg gag gtc ctt cct tgc tca cgg gtg gcc cac att gag cgg aag	830
Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile Glu Arg Lys	
240 245 250	
aag aag cca tat aat agc aac att ggc ttc tac acc aag agg aat gct	878
Lys Lys Pro Tyr Asn Ser Asn Ile Gly Phe Tyr Thr Lys Arg Asn Ala	
255 260 265	
ctt cgc gtt gct gag gtc tgg atg gac gat tac aag tct cat gtg tac	926
Leu Arg Val Ala Glu Val Trp Met Asp Asp Tyr Lys Ser His Val Tyr	
270 275 280	
ata gcg tgg aac ctg ccg ctg gag aat ccg gga att gac atc ggt gat	974
Ile Ala Trp Asn Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly Asp	
285 290 295 300	
gtc tcc gaa aga aga gca tta agg aaa agt tta aag tgt aag aat ttc	1022
Val Ser Glu Arg Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn Phe	
305 310 315	
cag tgg tac ctg gac cat gtt tac cca gaa atg aga aga tac aat aat	1070
Gln Trp Tyr Leu Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn Asn	
320 325 330	
acc gtt gct tac ggg gag ctt cgc aac aac aag gca aaa gac gtc tgc	1118
Thr Val Ala Tyr Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val Cys	
335 340 345	
ttg gac cag ggg ccg ctg gag aac cac aca gca ata ttg tat ccg tgc	1166
Leu Asp Gln Gly Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro Cys	
350 355 360	
cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc ctg	1214
His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu	
365 370 375 380	

cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc tgc	1262
His Leu Gly Ala Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys	
385 390 395	
ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc gac	1310
Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp	
400 405 410	
aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat gga	1358
Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly	
415 420 425	
gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac cgg	1406
Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg	
430 435 440	
ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag agg	1454
Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg	
445 450 455 460	
tgg acc att aag aac tcc atc aag tagagggagg gagctggggc actggagcct	1508
Trp Thr Ile Lys Asn Ser Ile Lys	
465	
ggccccccagg acatggctgc tccccccaac atctggacca gctgccctgg cggagagaca	1568
gcaagggggcc ggcaggtgct cgatggggccc cccagggtt ctccaggga gcacaggga	1628
cccggatgaa gactctgtcc cccctcaggc attcagctgc ccacaagttt cctgcaccct	1688
ggaaaagccc cccacccttc ctctgggaaa ctgacagctg tcttccacag cctctgatgt	1748
ggacctggta ctgaggagca agactgtcca gttctcctcc acatctccca tcccagaatc	1808
aggatctggg actggcaggg tcccctcctg tgtctcatct cttgcagcag cagctgctga	1868
actccagcca tcaacacggt gggaggcagc gggggcttca gccatgtcct agctccccgc	1928
cctaaaagga ggcagtgagg accaggcact atttctcctg aggttacttc taccagatg	1988
acacctgcct gttcacgccc caaggcagct actgccccta acccttccca ccagggtagc	2048
tttgggcact gcagctctgg acttttctgg cccctcctga gatgacctga tggagctgat	2108
gctttctctc ctaatccctg ggcactaggc tcttatcagt gtgcttgggc cagctctcct	2168
gcctgtgtct agaggaagcc agagacagaa ataggctaag cctgcagtag gatctcagcc	2228
acaagggccc cgcaggatgg agctgggtca aggaccaggg agccctgact cccagaggct	2288
gccaccgggg agaagcagcg gtctccatc cagaacctaa gggctgaagc aaaggctgcc	2348
aggacccttg aagatgcttt tggtcacct catttcaccc cagctctgc tggctggcag	2408
aggagaaggc agtcgtttcc tctctgaaga gtattttttt cgattgccct ctgggttaggg	2468
tgcacatata aatcagagtt aatatatgaa cgcgtgtgca tgcacaagtg tgtgtgtgcc	2528

tgcgtgctgt gcgtggcagg gtgtgtgtgt gtgtgtctgg ctgtgcgttc cggagtgtgt 2588
 gacgatgctg acctagctgt gcggccttgg gcttgcctgt tcattactca cctggatggg 2648
 gacgagggat gagaaggggtg tgggtttggc cccatgtcac tggccggaag gatgtgtctc 2708
 agccctgccc tgtgggggtgc ccccgatggg aggctgtccc atctcccagt ccccatctct 2768
 ttttccccac actgtccctg gccaaacct gccagagct gaacctgta gctgccccct 2828
 tgccctgtgt gggattcgca gtgtctcatt tgggtgacgtc ttactgggtga tcatctctc 2888
 acccatctc ccaccttgtg gaataaatac atgttagcac ttcccagagc agcctccttt 2948
 gtgtcttgat ttctccagaa ctggaggtgg ggaggggagt gatggagaca taggaggaga 3008
 gcttctttgg ctttgagggt ttagtgttac ttatttatct atttattcga gatgggggtct 3068
 tgctctgtgg cccaggctgg agtgacgtgg tgcaatcatg a 3109

<210> 70
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Lys Arg Arg Ser Gly Thr Pro Thr Thr Leu Cys Lys Glu Leu Lys
 1 5 10 15
 Tyr Ser Lys Asp Pro Pro Gln Ile Ser Ile Ile Phe Ile Phe Val Asn
 20 25 30
 Glu Ala Leu Ser Val Ile Leu Arg Ser Val His Ser Ala Val Asn His
 35 40 45
 Thr Pro Thr His Leu Leu Lys Glu Ile Ile Leu Val Asp Asp Asn Ser
 50 55 60
 Asp Glu Glu Glu Leu Lys Val Pro Leu Glu Glu Tyr Val His Lys Arg
 65 70 75 80
 Tyr Pro Gly Leu Val Lys Val Val Arg Asn Gln Lys Arg Glu Gly Leu
 85 90 95
 Ile Arg Ala Arg Ile Glu Gly Trp Lys Val Ala Thr Gly Gln Val Thr
 100 105 110
 Gly Phe Phe Asp Ala His Val Glu Phe Thr Ala Gly Trp Ala Glu Pro
 115 120 125
 Val Leu Ser Arg Ile Gln Glu Asn Arg Lys Arg Val Ile Leu Pro Ser
 130 135 140
 Ile Asp Asn Ile Lys Gln Asp Asn Phe Glu Val Gln Arg Tyr Glu Asn
 145 150 155 160

Ser Ala His Gly Tyr Ser Trp Glu Leu Trp Cys Met Tyr Ile Ser Pro
 165 170 175
 Pro Lys Asp Trp Trp Asp Ala Gly Asp Pro Ser Leu Pro Ile Arg Thr
 180 185 190
 Pro Ala Met Ile Gly Cys Ser Phe Val Val Asn Arg Lys Phe Phe Gly
 195 200 205
 Glu Ile Gly Leu Leu Asp Pro Gly Met Asp Val Tyr Gly Gly Glu Asn
 210 215 220
 Ile Glu Leu Gly Ile Lys Val Trp Leu Cys Gly Gly Ser Met Glu Val
 225 230 235 240
 Leu Pro Cys Ser Arg Val Ala His Ile Glu Arg Lys Lys Lys Pro Tyr
 245 250 255
 Asn Ser Asn Ile Gly Phe Tyr Thr Lys Arg Asn Ala Leu Arg Val Ala
 260 265 270
 Glu Val Trp Met Asp Asp Tyr Lys Ser His Val Tyr Ile Ala Trp Asn
 275 280 285
 Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly Asp Val Ser Glu Arg
 290 295 300
 Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn Phe Gln Trp Tyr Leu
 305 310 315 320
 Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn Asn Thr Val Ala Tyr
 325 330 335
 Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val Cys Leu Asp Gln Gly
 340 345 350
 Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro Cys His Gly Trp Gly
 355 360 365
 Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe Leu His Leu Gly Ala
 370 375 380
 Leu Gly Thr Thr Thr Leu Leu Pro Asp Thr Arg Cys Leu Val Asp Asn
 385 390 395 400
 Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys Asp Lys Val Lys Ser
 405 410 415
 Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn Gly Ala Ile Met Asn
 420 425 430
 Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn Arg Gly Leu Ala Gly
 435 440 445
 Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln Arg Trp Thr Ile Lys
 450 455 460

Asn Ser Ile Lys
465

<210> 71
<211> 1066
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(1057)

```

<400> 71
c acc gga tcc atg aag gat tgc agt aac gga tgc tcc gca gag tgt acc 49
  Thr Gly Ser Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr
    1             5             10             15

gga gaa gga gga tca aaa gag gtg gtg ggg act ttt aag gct aaa gac 97
Gly Glu Gly Gly Ser Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp
    20             25             30

cta ata gtc aca cca gct acc att tta aag gaa aaa cca gac ccc aat 145
Leu Ile Val Thr Pro Ala Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn
    35             40             45

aat ctg gtt ttt gga act gtg ttc acg gat cat atg ctg acg gtg gag 193
Asn Leu Val Phe Gly Thr Val Phe Thr Asp His Met Leu Thr Val Glu
    50             55             60

tgg tcc tca gag ttt gga tgg gag aaa cct cat atc aag cct ctt cag 241
Trp Ser Ser Glu Phe Gly Trp Glu Lys Pro His Ile Lys Pro Leu Gln
    65             70             75             80

aac ctg tca ttg cac cct ggc tca tca gct ttg cac tat gca gtg gaa 289
Asn Leu Ser Leu His Pro Gly Ser Ser Ala Leu His Tyr Ala Val Glu
    85             90             95

gta ttt gac aaa gaa gag ctc tta gag tgt att caa cag ctt gtg aaa 337
Val Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile Gln Gln Leu Val Lys
    100            105            110

ttg gat caa gaa tgg gtc cca tat tca aca tct gct agt ctg tat att 385
Leu Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu Tyr Ile
    115            120            125

cgt cct aca ttc att gga act gag cct tct ctt gga gtc aag aag cct 433
Arg Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys Lys Pro
    130            135            140

acc aaa gcc ctg ctc ttt gta ctc ttg agc cca gtg gga cct tat ttt 481
Thr Lys Ala Leu Leu Phe Val Leu Leu Ser Pro Val Gly Pro Tyr Phe
    145            150            155            160

tca agt gga acc ttt aat cca gtg tcc ctg tgg gcc aat ccc aag tat 529
Ser Ser Gly Thr Phe Asn Pro Val Ser Leu Trp Ala Asn Pro Lys Tyr
    165            170            175

```

gta aga gcc tgg aaa ggt gga act ggg gac tgc aag atg gga ggg aat	577
Val Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly Gly Asn	
180 185 190	
tac ggc tca tct ctt ttt gcc caa tgt gaa gca gta gat aat ggg tgt	625
Tyr Gly Ser Ser Leu Phe Ala Gln Cys Glu Ala Val Asp Asn Gly Cys	
195 200 205	
cag cag gtc ctg tgg ctc tat gga gag gac cat cag atc act gaa gtg	673
Gln Gln Val Leu Trp Leu Tyr Gly Glu Asp His Gln Ile Thr Glu Val	
210 215 220	
gga act atg aat ctt ttt ctt tac tgg ata aat gaa gat gga gaa gaa	721
Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly Glu Glu	
225 230 235 240	
gaa ctg gca act cct cca cta gat ggc atc att ctt cca gga gtg aca	769
Glu Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile Leu Pro Gly Val Thr	
245 250 255	
agg cgg tgc att ctg gac ctg gca cat cag tgg ggt gaa ttt aag gtg	817
Arg Arg Cys Ile Leu Asp Leu Ala His Gln Trp Gly Glu Phe Lys Val	
260 265 270	
tca gag aga tac ctc acc atg gat gac ttg aca aca gcc ctg gag ggg	865
Ser Glu Arg Tyr Leu Thr Met Asp Asp Leu Thr Thr Ala Leu Glu Gly	
275 280 285	
aac aga gtg aga gag atg ttt ggc tct ggt aca gcc tgt gtt gtt tgc	913
Asn Arg Val Arg Glu Met Phe Gly Ser Gly Thr Ala Cys Val Val Cys	
290 295 300	
cca gtt tct gat ata ctg tac aaa ggc gag aca ata cac att cca act	961
Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile Pro Thr	
305 310 315 320	
atg gag aat ggt cct aag ctg gca agc cgc atc ttg agc aaa tta act	1009
Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys Leu Thr	
325 330 335	
gat atc cag tat gga aga gaa gag agc gac tgg aca att gtg cta tcc	1057
Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val Leu Ser	
340 345 350	
gtcgacggc	1066
<210> 72	
<211> 352	
<212> PRT	
<213> Homo sapiens	
<400> 72	
Thr Gly Ser Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr	
1 5 10 15	
Gly Glu Gly Gly Ser Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp	
20 25 30	

Leu	Ile	Val	Thr	Pro	Ala	Thr	Ile	Leu	Lys	Glu	Lys	Pro	Asp	Pro	Asn	35	40	45	
Asn	Leu	Val	Phe	Gly	Thr	Val	Phe	Thr	Asp	His	Met	Leu	Thr	Val	Glu	50	55	60	
Trp	Ser	Ser	Glu	Phe	Gly	Trp	Glu	Lys	Pro	His	Ile	Lys	Pro	Leu	Gln	65	70	75	80
Asn	Leu	Ser	Leu	His	Pro	Gly	Ser	Ser	Ala	Leu	His	Tyr	Ala	Val	Glu	85	90	95	
Val	Phe	Asp	Lys	Glu	Glu	Leu	Leu	Glu	Cys	Ile	Gln	Gln	Leu	Val	Lys	100	105	110	
Leu	Asp	Gln	Glu	Trp	Val	Pro	Tyr	Ser	Thr	Ser	Ala	Ser	Leu	Tyr	Ile	115	120	125	
Arg	Pro	Thr	Phe	Ile	Gly	Thr	Glu	Pro	Ser	Leu	Gly	Val	Lys	Lys	Pro	130	135	140	
Thr	Lys	Ala	Leu	Leu	Phe	Val	Leu	Leu	Ser	Pro	Val	Gly	Pro	Tyr	Phe	145	150	155	160
Ser	Ser	Gly	Thr	Phe	Asn	Pro	Val	Ser	Leu	Trp	Ala	Asn	Pro	Lys	Tyr	165	170	175	
Val	Arg	Ala	Trp	Lys	Gly	Gly	Thr	Gly	Asp	Cys	Lys	Met	Gly	Gly	Asn	180	185	190	
Tyr	Gly	Ser	Ser	Leu	Phe	Ala	Gln	Cys	Glu	Ala	Val	Asp	Asn	Gly	Cys	195	200	205	
Gln	Gln	Val	Leu	Trp	Leu	Tyr	Gly	Glu	Asp	His	Gln	Ile	Thr	Glu	Val	210	215	220	
Gly	Thr	Met	Asn	Leu	Phe	Leu	Tyr	Trp	Ile	Asn	Glu	Asp	Gly	Glu	Glu	225	230	235	240
Glu	Leu	Ala	Thr	Pro	Pro	Leu	Asp	Gly	Ile	Ile	Leu	Pro	Gly	Val	Thr	245	250	255	
Arg	Arg	Cys	Ile	Leu	Asp	Leu	Ala	His	Gln	Trp	Gly	Glu	Phe	Lys	Val	260	265	270	
Ser	Glu	Arg	Tyr	Leu	Thr	Met	Asp	Asp	Leu	Thr	Thr	Ala	Leu	Glu	Gly	275	280	285	
Asn	Arg	Val	Arg	Glu	Met	Phe	Gly	Ser	Gly	Thr	Ala	Cys	Val	Val	Cys	290	295	300	
Pro	Val	Ser	Asp	Ile	Leu	Tyr	Lys	Gly	Glu	Thr	Ile	His	Ile	Pro	Thr	305	310	315	320
Met	Glu	Asn	Gly	Pro	Lys	Leu	Ala	Ser	Arg	Ile	Leu	Ser	Lys	Leu	Thr	325	330	335	

Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val Leu Ser
 340 345 350

<210> 73
 <211> 2043
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (528)..(1685)

<400> 73
 agtagggagg tgggcaggag ccagtgatga cggaatggca atcacatttg acctctgatc 60
 tgtttatttc ctctccttg acgtctccat ataaatgtta cacgggcatc cccacactcg 120
 gatacgacc cacagtggct gattcggggg taaccgtgtc atttgcttgc aacactggca 180
 cctctgccct gcacccggg agtgagcagt gagtgaggct cgggtctggg cgctggctcc 240
 gaatcttcgg gctgggagag actccaccat ctgggggcgg cctgggggag cagccttagt 300
 gtcttctgc tgatgcaatc cgctaggtcg cgagtctccg ccgcgagagg gccgggtctgc 360
 aatccagccc gccacgtgta ctgcgcgcg cctcgggcac tgccccaggt cttgctgcag 420
 ccgggaccgc gctctgcagc cgcagaccgc gtccacacgg ccaggggcta cgacccttgg 480
 gatctgccct ccgctcagct cgagcttccc tcgtggccga cggaaca atg aag gat 536
 Met Lys Asp
 1
 tgc agt aac gga tgc tcc gca gag tgt acc gga gaa gga gga tca aaa 584
 Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr Gly Glu Gly Gly Ser Lys
 5 10 15
 gag gtg gtg ggg act ttt aag gct aaa gac cta ata gtc aca cca gct 632
 Glu Val Val Gly Thr Phe Lys Ala Lys Asp Leu Ile Val Thr Pro Ala
 20 25 30 35
 acc att tta aag gaa aaa cca gac ccc aat aat ctg gtt ttt gga act 680
 Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn Asn Leu Val Phe Gly Thr
 40 45 50
 gtg ttc acg gat cat atg ctg acg gtg gag tgg tcc tca gag ttt gga 728
 Val Phe Thr Asp His Met Leu Thr Val Glu Trp Ser Ser Glu Phe Gly
 55 60 65
 tgg gag aaa cct cat atc aag cct ctt cag aac ctg tca ttg cac cct 776
 Trp Glu Lys Pro His Ile Lys Pro Leu Gln Asn Leu Ser Leu His Pro
 70 75 80
 ggc tca tca gct ttg cac tat gca gtg gaa tta ttt gaa gga ttg aag 824
 Gly Ser Ser Ala Leu His Tyr Ala Val Glu Leu Phe Glu Gly Leu Lys
 85 90 95

gca ttt cga gga gta gat aat aaa att cga ctg ttt cag cca aac ctc	872
Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu Phe Gln Pro Asn Leu	
100 105 110 115	
aac atg gat aga atg tat cgc tct gct gtg agg gca act ctg ccg gta	920
Asn Met Asp Arg Met Tyr Arg Ser Ala Val Arg Ala Thr Leu Pro Val	
120 125 130	
ttt gac aaa gaa gag ctc tta gag tgt att caa cag ctt gtg aaa ttg	968
Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile Gln Gln Leu Val Lys Leu	
135 140 145	
gat caa gaa tgg gtc cca tat tca aca tct gct agt ctg tat att cgt	1016
Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu Tyr Ile Arg	
150 155 160	
cct aca ttc att gga act gag cct tct ctt gga gtc aag aag cct acc	1064
Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys Lys Pro Thr	
165 170 175	
aaa gcc ctg ctc ttt gta ctc ttg agc cca gtg gga cct tat ttt tca	1112
Lys Ala Leu Leu Phe Val Leu Leu Ser Pro Val Gly Pro Tyr Phe Ser	
180 185 190 195	
agt gga acc ttt aat cca gtg tcc ctg tgg gcc aat ccc aag tat gta	1160
Ser Gly Thr Phe Asn Pro Val Ser Leu Trp Ala Asn Pro Lys Tyr Val	
200 205 210	
aga gcc tgg aaa ggt gga act ggg gac tgc aag atg gga ggg aat tac	1208
Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly Gly Asn Tyr	
215 220 225	
ggc tca tct ctt ttt gcc caa tgt gaa gca gta gat aat ggg tgt cag	1256
Gly Ser Ser Leu Phe Ala Gln Cys Glu Ala Val Asp Asn Gly Cys Gln	
230 235 240	
cag gtc ctg tgg ctc tat gga gag gac cat cag atc act gaa gtg gga	1304
Gln Val Leu Trp Leu Tyr Gly Glu Asp His Gln Ile Thr Glu Val Gly	
245 250 255	
act atg aat ctt ttt ctt tac tgg ata aat gaa gat gga gaa gaa gaa	1352
Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly Glu Glu Glu	
260 265 270 275	
ctg gca act cct cca cta gat ggc atc att ctt cca gga gtg aca agg	1400
Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile Leu Pro Gly Val Thr Arg	
280 285 290	
cgg tgc att ctg gac ctg gca cat cag tgg ggt gaa ttt aag gtg tca	1448
Arg Cys Ile Leu Asp Leu Ala His Gln Trp Gly Glu Phe Lys Val Ser	
295 300 305	
gag aga tac ctc acc atg gat gac ttg tca aca gcc ctg gag ggg aac	1496
Glu Arg Tyr Leu Thr Met Asp Asp Leu Ser Thr Ala Leu Glu Gly Asn	
310 315 320	

aga gtg aga gag atg ttt ggc tct ggt aca gcc tgt gtt gtt tgc cca 1544
 Arg Val Arg Glu Met Phe Gly Ser Gly Thr Ala Cys Val Val Cys Pro
 325 330 335

gtt tct gat ata ctg tac aaa ggc gag aca ata cac att cca act atg 1592
 Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile Pro Thr Met
 340 345 350 355

gag aat ggt cct aag ctg gca agc cgc atc ttg agc aaa tta act gat 1640
 Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys Leu Thr Asp
 360 365 370

atc cag tat gga aga gaa gag agc gac tgg aca att gtg cta tcc 1685
 Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val Leu Ser
 375 380 385

tgaatggaaa atagaggata caatggaaaa tagaggatac caactgtatg ctactgggac 1745

agactgttgc atttgaattg tgatagattt ctttggctac ctgtgcataa tgtagtttgt 1805

agtatcaatg tgttacaaga gtgattgttt cttcatgcc a gagaaaatga attgcaatca 1865

tcaaatggtg tttcataact tggtagtagt aacttacctt accttaccta gaaaaatatt 1925

aatgtaagcc atataacatg ggattttcct caatgatttt agtgcctcct tttgtacttc 1985

actcagatac taaatagtag tttattcttt aatataagtt acattctgct cctcaacc 2043

<210> 74

<211> 386

<212> PRT

<213> Homo sapiens

<400> 74

Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr Gly Glu Gly
 1 5 10 15

Gly Ser Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp Leu Ile Val
 20 25 30

Thr Pro Ala Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn Asn Leu Val
 35 40 45

Phe Gly Thr Val Phe Thr Asp His Met Leu Thr Val Glu Trp Ser Ser
 50 55 60

Glu Phe Gly Trp Glu Lys Pro His Ile Lys Pro Leu Gln Asn Leu Ser
 65 70 75 80

Leu His Pro Gly Ser Ser Ala Leu His Tyr Ala Val Glu Leu Phe Glu
 85 90 95

Gly Leu Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu Phe Gln
 100 105 110

Pro Asn Leu Asn Met Asp Arg Met Tyr Arg Ser Ala Val Arg Ala Thr
 115 120 125

Leu Pro Val Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile Gln Gln Leu
 130 135 140
 Val Lys Leu Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu
 145 150 155 160
 Tyr Ile Arg Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys
 165 170 175
 Lys Pro Thr Lys Ala Leu Leu Phe Val Leu Leu Ser Pro Val Gly Pro
 180 185 190
 Tyr Phe Ser Ser Gly Thr Phe Asn Pro Val Ser Leu Trp Ala Asn Pro
 195 200 205
 Lys Tyr Val Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly
 210 215 220
 Gly Asn Tyr Gly Ser Ser Leu Phe Ala Gln Cys Glu Ala Val Asp Asn
 225 230 235 240
 Gly Cys Gln Gln Val Leu Trp Leu Tyr Gly Glu Asp His Gln Ile Thr
 245 250 255
 Glu Val Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly
 260 265 270
 Glu Glu Glu Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile Leu Pro Gly
 275 280 285
 Val Thr Arg Arg Cys Ile Leu Asp Leu Ala His Gln Trp Gly Glu Phe
 290 295 300
 Lys Val Ser Glu Arg Tyr Leu Thr Met Asp Asp Leu Ser Thr Ala Leu
 305 310 315 320
 Glu Gly Asn Arg Val Arg Glu Met Phe Gly Ser Gly Thr Ala Cys Val
 325 330 335
 Val Cys Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile
 340 345 350
 Pro Thr Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys
 355 360 365
 Leu Thr Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val
 370 375 380
 Leu Ser
 385
 <210> 75
 <211> 1177
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11)..(1168)

 <400> 75
 caccg gatcc atg aag gat tgc agt aac gga tgc tcc gca gag tgt acc 49
 Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr
 1 5 10

 gga gaa gga gga tca aaa gag gtg gtg ggg act ttt aag gct aaa gac 97
 Gly Glu Gly Gly Ser Lys Glu Val Val Gly Thr Phe Lys Ala Lys Asp
 15 20 25

 cta ata gtc aca cca gct acc att tta aag gaa aaa cca gac ccc aat 145
 Leu Ile Val Thr Pro Ala Thr Ile Leu Lys Glu Lys Pro Asp Pro Asn
 30 35 40 45

 aat ctg gtt ttt gga act gtg ttc acg gat cat atg ctg acg gtg gag 193
 Asn Leu Val Phe Gly Thr Val Phe Thr Asp His Met Leu Thr Val Glu
 50 55 60

 tgg tcc tca gag ttt gga tgg gag aaa cct cat atc aag cct ctt cag 241
 Trp Ser Ser Glu Phe Gly Trp Glu Lys Pro His Ile Lys Pro Leu Gln
 65 70 75

 aac ctg tca ttg cac cct ggc tca tca gct ttg cac tat gca gtg gaa 289
 Asn Leu Ser Leu His Pro Gly Ser Ser Ala Leu His Tyr Ala Val Glu
 80 85 90

 tta ttt gaa gga ttg aag gca ttt cga gga gta gat aat aaa att cga 337
 Leu Phe Glu Gly Leu Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg
 95 100 105

 ctg ttt cag cca aac ctc aac atg gat aga atg tat cgc tct gct gtg 385
 Leu Phe Gln Pro Asn Leu Asn Met Asp Arg Met Tyr Arg Ser Ala Val
 110 115 120 125

 agg gca act ctg ccg gta ttt gac aaa gaa gag ctc tta gag tgt att 433
 Arg Ala Thr Leu Pro Val Phe Asp Lys Glu Glu Leu Leu Glu Cys Ile
 130 135 140

 caa cag ctt gtg aaa ttg gat caa gaa tgg gtc cca tat tca aca tct 481
 Gln Gln Leu Val Lys Leu Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser
 145 150 155

 gct agt ctg tat att cgt cct aca ttc att gga act gag cct tct ctt 529
 Ala Ser Leu Tyr Ile Arg Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu
 160 165 170

 gga gtc aag aag cct acc aaa gcc ctg ctc ttt gta ctc ttg agc cca 577
 Gly Val Lys Lys Pro Thr Lys Ala Leu Leu Phe Val Leu Leu Ser Pro
 175 180 185

 gtg gga cct tat ttt tca agt gga acc ttt aat cca gtg tcc ctg tgg 625
 Val Gly Pro Tyr Phe Ser Ser Gly Thr Phe Asn Pro Val Ser Leu Trp
 190 195 200 205

gcc aat ccc aag tat gta aga gcc tgg aaa ggt gga act ggg gac tgc	673
Ala Asn Pro Lys Tyr Val Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys	
210 215 220	
aag atg gga ggg aat tac ggc tca tct ctt ttt gcc caa tgt gaa gca	721
Lys Met Gly Gly Asn Tyr Gly Ser Ser Leu Phe Ala Gln Cys Glu Ala	
225 230 235	
gta gat aat ggg tgt cag cag gtc ctg tgg ctc tat gga gag gac cat	769
Val Asp Asn Gly Cys Gln Gln Val Leu Trp Leu Tyr Gly Glu Asp His	
240 245 250	
cag atc act gaa gtg gga act atg aat ctt ttt ctt tac tgg ata aat	817
Gln Ile Thr Glu Val Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn	
255 260 265	
gaa gat gga gaa gaa gaa ctg gca act cct cca cta gat ggc atc att	865
Glu Asp Gly Glu Glu Glu Leu Ala Thr Pro Pro Leu Asp Gly Ile Ile	
270 275 280 285	
ctt cca gga gtg aca agg cgg tgc att ctg gac ctg gca cat cag tgg	913
Leu Pro Gly Val Thr Arg Arg Cys Ile Leu Asp Leu Ala His Gln Trp	
290 295 300	
ggt gaa ttt aag gtg tca gag aga tac ctc acc atg gat gac ttg aca	961
Gly Glu Phe Lys Val Ser Glu Arg Tyr Leu Thr Met Asp Asp Leu Thr	
305 310 315	
aca gcc ctg gag ggg aac aga gtg aga gag atg ttt ggc tct ggt aca	1009
Thr Ala Leu Glu Gly Asn Arg Val Arg Glu Met Phe Gly Ser Gly Thr	
320 325 330	
gcc tgt gtt gtt tgc cca gtt tct gat ata ctg tac aaa ggc gag aca	1057
Ala Cys Val Val Cys Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr	
335 340 345	
ata cac att cca act atg gag aat ggt cct aag ctg gca agc cgc atc	1105
Ile His Ile Pro Thr Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile	
350 355 360 365	
ttg agc aaa tta act gat atc cag tat gga aga gaa gag agc gac tgg	1153
Leu Ser Lys Leu Thr Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp	
370 375 380	
aca att gtg cta tcc gtcgacggc	1177
Thr Ile Val Leu Ser	
385	
<210> 76	
<211> 386	
<212> PRT	
<213> Homo sapiens	
<400> 76	
Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Glu Cys Thr Gly Glu Gly	
1 5 10 15	

Gly	Ser	Lys	Glu	Val	Val	Gly	Thr	Phe	Lys	Ala	Lys	Asp	Leu	Ile	Val		
			20					25					30				
Thr	Pro	Ala	Thr	Ile	Leu	Lys	Glu	Lys	Pro	Asp	Pro	Asn	Asn	Leu	Val		
		35					40					45					
Phe	Gly	Thr	Val	Phe	Thr	Asp	His	Met	Leu	Thr	Val	Glu	Trp	Ser	Ser		
	50					55					60						
Glu	Phe	Gly	Trp	Glu	Lys	Pro	His	Ile	Lys	Pro	Leu	Gln	Asn	Leu	Ser		
65					70					75					80		
Leu	His	Pro	Gly	Ser	Ser	Ala	Leu	His	Tyr	Ala	Val	Glu	Leu	Phe	Glu		
				85					90					95			
Gly	Leu	Lys	Ala	Phe	Arg	Gly	Val	Asp	Asn	Lys	Ile	Arg	Leu	Phe	Gln		
			100					105					110				
Pro	Asn	Leu	Asn	Met	Asp	Arg	Met	Tyr	Arg	Ser	Ala	Val	Arg	Ala	Thr		
		115					120					125					
Leu	Pro	Val	Phe	Asp	Lys	Glu	Glu	Leu	Leu	Glu	Cys	Ile	Gln	Gln	Leu		
	130					135					140						
Val	Lys	Leu	Asp	Gln	Glu	Trp	Val	Pro	Tyr	Ser	Thr	Ser	Ala	Ser	Leu		
145					150					155					160		
Tyr	Ile	Arg	Pro	Thr	Phe	Ile	Gly	Thr	Glu	Pro	Ser	Leu	Gly	Val	Lys		
				165				170						175			
Lys	Pro	Thr	Lys	Ala	Leu	Leu	Phe	Val	Leu	Leu	Ser	Pro	Val	Gly	Pro		
			180					185					190				
Tyr	Phe	Ser	Ser	Gly	Thr	Phe	Asn	Pro	Val	Ser	Leu	Trp	Ala	Asn	Pro		
		195					200					205					
Lys	Tyr	Val	Arg	Ala	Trp	Lys	Gly	Gly	Thr	Gly	Asp	Cys	Lys	Met	Gly		
	210					215					220						
Gly	Asn	Tyr	Gly	Ser	Ser	Leu	Phe	Ala	Gln	Cys	Glu	Ala	Val	Asp	Asn		
225					230					235					240		
Gly	Cys	Gln	Gln	Val	Leu	Trp	Leu	Tyr	Gly	Glu	Asp	His	Gln	Ile	Thr		
				245					250					255			
Glu	Val	Gly	Thr	Met	Asn	Leu	Phe	Leu	Tyr	Trp	Ile	Asn	Glu	Asp	Gly		
			260					265					270				
Glu	Glu	Glu	Leu	Ala	Thr	Pro	Pro	Leu	Asp	Gly	Ile	Ile	Leu	Pro	Gly		
		275					280					285					
Val	Thr	Arg	Arg	Cys	Ile	Leu	Asp	Leu	Ala	His	Gln	Trp	Gly	Glu	Phe		
	290					295					300						
Lys	Val	Ser	Glu	Arg	Tyr	Leu	Thr	Met	Asp	Asp	Leu	Thr	Thr	Ala	Leu		
305					310					315					320		

Glu Gly Asn Arg Val Arg Glu Met Phe Gly Ser Gly Thr Ala Cys Val
 325 330 335

Val Cys Pro Val Ser Asp Ile Leu Tyr Lys Gly Glu Thr Ile His Ile
 340 345 350

Pro Thr Met Glu Asn Gly Pro Lys Leu Ala Ser Arg Ile Leu Ser Lys
 355 360 365

Leu Thr Asp Ile Gln Tyr Gly Arg Glu Glu Ser Asp Trp Thr Ile Val
 370 375 380

Leu Ser
 385

<210> 77

<211> 1057

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11) .. (1048)

<400> 77

caccagatct atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac acc 49
 Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr
 1 5 10

atc tcc cag gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc 97
 Ile Ser Gln Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly
 15 20 25

gca cta ggc aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag 145
 Ala Leu Gly Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys
 30 35 40 45

acc tgg aag ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat 193
 Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp
 50 55 60

ttc ctc ctt atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga 241
 Phe Leu Leu Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg
 65 70 75

cgt aga cac tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc 289
 Arg Arg His Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe
 80 85 90

acg ttg gcc atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg 337
 Thr Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val
 95 100 105

gct gcg gac agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac 385
 Ala Ala Asp Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn
 110 115 120 125

act atc tcc acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc	433
Thr Ile Ser Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala	
130 135 140	
ctg gtc atc ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc	481
Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Glu Asn His Leu Cys	
145 150 155	
gtg caa gag acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc	529
Val Gln Glu Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala	
160 165 170	
aat ggc tgg cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc	577
Asn Gly Trp His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu	
175 180 185	
ggc atc atc tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg	625
Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg	
190 195 200 205	
agg cag cag ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc	673
Arg Gln Gln Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe	
210 215 220	
atc atg gtg gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg	721
Ile Met Val Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val	
225 230 235	
tct gct aga ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat	769
Ser Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp	
240 245 250	
ccc tct gtc cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg	817
Pro Ser Val His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met	
255 260 265	
aac agc atg ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt	865
Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe	
270 275 280 285	
ccc aaa ttc tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag	913
Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln	
290 295 300	
cca gga cac tca aaa aca caa agg ccg gaa gag atg cca att tcg aac	961
Pro Gly His Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn	
305 310 315	
ctc ggt cgc agg agt tgc atc agt gtg gca aat agt ttc caa agc cag	1009
Leu Gly Arg Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln	
320 325 330	
tct gat ggg caa tgg gat ccc cac att gtt gag tgg cac aagcttggc	1057
Ser Asp Gly Gln Trp Asp Pro His Ile Val Glu Trp His	
335 340 345	

<210> 78

<211> 346
 <212> PRT
 <213> Homo sapiens

<400> 78

Met	Tyr	Asn	Gly	Ser	Cys	Cys	Arg	Ile	Glu	Gly	Asp	Thr	Ile	Ser	Gln
1				5					10					15	
Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	Gly	Ala	Leu	Gly
			20					25					30		
Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys	Thr	Trp	Lys
	35						40					45			
Pro	Ser	Thr	Val	Tyr	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu
	50					55					60				
Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His
65					70				75						80
Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala
				85					90					95	
Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Asp
			100					105					110		
Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	Thr	Ile	Ser
		115					120					125			
Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile
	130					135					140				
Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys	Val	Gln	Glu
145					150				155					160	
Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala	Asn	Gly	Trp
				165					170					175	
His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu	Gly	Ile	Ile
			180					185					190		
Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	Arg	Gln	Gln
		195					200					205			
Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val
	210					215					220				
Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg
225					230					235					240
Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val
			245						250					255	
His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met
		260						265					270		
Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe

275	280	285	
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His			
290	295	300	
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg			
305	310	315	320
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly			
	325	330	335
Gln Trp Asp Pro His Ile Val Glu Trp His			
	340	345	
<210> 79			
<211> 961			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (2) .. (961)			
<400> 79			
c acc tcg cga aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag			49
Thr Ser Arg Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys			
1	5	10	15
acc tgg aag ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat			97
Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp			
	20	25	30
ttc ctc ctt atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga			145
Phe Leu Leu Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg			
	35	40	45
cgt aga cac tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc			193
Arg Arg His Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe			
	50	55	60
acg ttg gcc atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg			241
Thr Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val			
	65	70	75
gct gcg gac agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac			289
Ala Ala Asp Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn			
	85	90	95
act atc tcc acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc			337
Thr Ile Ser Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala			
	100	105	110
ctg gtc atc ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc			385
Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys			
	115	120	125
gtg caa gag acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc			433

Val	Gln	Glu	Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala		
130						135					140						
aat	ggc	tgg	cat	gac	atc	atg	ttc	cag	ctg	gag	ttc	ttt	atg	ccc	ctc	481	
Asn	Gly	Trp	His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu		
145					150					155					160		
ggc	atc	atc	tta	ttt	tgc	tcc	ttc	aag	att	gtt	tgg	agc	ctg	agg	cgg	529	
Gly	Ile	Ile	Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg		
				165					170						175		
agg	cag	cag	ctg	gcc	aga	cag	gct	cgg	atg	aag	aag	gcg	acc	cgg	ttc	577	
Arg	Gln	Gln	Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe		
			180					185					190				
atc	atg	gtg	gtg	gca	att	gtg	ttc	atc	aca	tgc	tac	ctg	ccc	agc	gtg	625	
Ile	Met	Val	Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val		
		195					200					205					
tct	gct	aga	ctc	tat	ttc	ctc	tgg	acg	gtg	ccc	tcg	agt	gcc	tgc	gat	673	
Ser	Ala	Arg	Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp		
	210					215				220							
ccc	tct	gtc	cat	ggg	gcc	ctg	cac	ata	acc	ctc	agc	ttc	acc	tac	atg	721	
Pro	Ser	Val	His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met		
225					230					235					240		
aac	agc	atg	ctg	gat	ccc	ctg	gtg	tat	tat	ttt	tca	agc	ccc	tcc	ttt	769	
Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe		
				245				250						255			
ccc	aaa	ttc	tac	aac	aag	ctc	aaa	atc	tgc	agt	ctg	aaa	ccc	aag	cag	817	
Pro	Lys	Phe	Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln		
			260					265					270				
cca	gga	cac	tca	aaa	aca	caa	agg	ccg	gaa	gag	atg	cca	att	tcg	aac	865	
Pro	Gly	His	Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn		
			275				280					285					
ctc	ggt	cgc	agg	agt	tgc	atc	agt	gtg	gca	aat	agt	ttc	caa	agc	cag	913	
Leu	Gly	Arg	Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	Gln		
	290					295				300							
tct	gat	ggg	caa	tgg	gat	ccc	cac	att	gtt	gag	tgg	cac	gtc	gac	ggc	961	
Ser	Asp	Gly	Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His	Val	Asp	Gly		
305					310					315					320		
<210> 80																	
<211> 320																	
<212> PRT																	
<213> Homo sapiens																	
<400> 80																	
Thr	Ser	Arg	Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys		
1				5					10					15			
Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp																	

20					25					30					
Phe	Leu	Leu	Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg
		35					40					45			
Arg	Arg	His	Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe
		50				55					60				
Thr	Leu	Ala	Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val
		65				70					75				80
Ala	Ala	Asp	Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn
				85					90					95	
Thr	Ile	Ser	Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala
			100					105					110		
Leu	Val	Ile	Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys
		115					120					125			
Val	Gln	Glu	Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala
		130					135					140			
Asn	Gly	Trp	His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu
		145				150					155				160
Gly	Ile	Ile	Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg
			165					170						175	
Arg	Gln	Gln	Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe
			180					185					190		
Ile	Met	Val	Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val
		195					200					205			
Ser	Ala	Arg	Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp
		210				215					220				
Pro	Ser	Val	His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met
		225				230					235				240
Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe
			245					250					255		
Pro	Lys	Phe	Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln
		260					265						270		
Pro	Gly	His	Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn
		275					280					285			
Leu	Gly	Arg	Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	Gln
		290				295					300				
Ser	Asp	Gly	Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His	Val	Asp	Gly
		305				310					315				320

<210> 81

<211> 1050
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (6)..(1043)

<400> 81

tcgcc atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac acc atc tcc	50
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser	
1 5 10 15	
cag gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta	98
Gln Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu	
20 25 30	
ggc aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg	146
Gly Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp	
35 40 45	
aag ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc	194
Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu	
50 55 60	
ctt atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga	242
Leu Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg	
65 70 75	
cac tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg	290
His Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu	
80 85 90 95	
gcc atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg	338
Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala	
100 105 110	
gac agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc	386
Asp Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile	
115 120 125	
tcc acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc	434
Ser Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val	
130 135 140	
atc ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa	482
Ile Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln	
145 150 155	
gag acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc	530
Glu Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly	
160 165 170 175	
tgg cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc	578
Trp His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile	
180 185 190	

atc tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag	626
Ile Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln	
195 200 205	
cag ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg	674
Gln Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met	
210 215 220	
gtg gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct	722
Val Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala	
225 230 235	
aga ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct	770
Arg Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser	
240 245 250 255	
gtc cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc	818
Val His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser	
260 265 270	
atg ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa	866
Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys	
275 280 285	
ttc tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga	914
Phe Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly	
290 295 300	
cac tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt	962
His Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly	
305 310 315	
cgc agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat	1010
Arg Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp	
320 325 330 335	
ggg caa tgg gat ccc cac att gtt gag tgg cac tgaacaa	1050
Gly Gln Trp Asp Pro His Ile Val Glu Trp His	
340 345	

<210> 82

<211> 346

<212> PRT

<213> Homo sapiens

<400> 82

Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
1 5 10 15

Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
20 25 30

Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
35 40 45

Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60

Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His	65	70	75	80
Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala	85	90	95	
Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Asp	100	105	110	
Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	Thr	Ile	Ser	115	120	125	
Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile	130	135	140	
Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys	Val	Gln	Glu	145	150	155	160
Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala	Asn	Gly	Trp	165	170	175	
His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu	Gly	Ile	Ile	180	185	190	
Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	Arg	Gln	Gln	195	200	205	
Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val	210	215	220	
Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg	225	230	235	240
Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val	245	250	255	
His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met	260	265	270	
Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe	275	280	285	
Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln	Pro	Gly	His	290	295	300	
Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn	Leu	Gly	Arg	305	310	315	320
Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	Gln	Ser	Asp	Gly	325	330	335	
Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His							340	345		

<210> 83
<211> 1104

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(1097)

<400> 83

```

gtgccattgt ggggactccc tgggctgctc tgcacccgga cacttgctct gtccccgcc 59

atg tac aac ggg tgc tgc tgc cgc atc gag ggg gac acc atc tcc cag 107
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
  1          5          10          15

gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta ggc 155
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
          20          25          30

aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag 203
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
          35          40          45

ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt 251
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
          50          55          60

atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac 299
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
  65          70          75          80

tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc 347
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
          85          90          95

atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg ggc 395
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Gly
          100          105          110

agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc 443
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
          115          120          125

acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc 491
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
          130          135          140

ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag 539
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
          145          150          155          160

acg gcc gtc tcc tgt gag agc ttc atc atg gag tgc gcc aat ggc tgg 587
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
          165          170          175

cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc 635
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
          180          185          190

```

tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg agg cag cag	683
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln	
195 200 205	
ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc atc atg gtg	731
Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val	
210 215 220	
gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg tct gct aga	779
Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg	
225 230 235 240	
ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat ccc tct gtc	827
Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val	
245 250 255	
cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg aac agc atg	875
His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met	
260 265 270	
ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt ccc aaa ttc	923
Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe	
275 280 285	
tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag cca gga cac	971
Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His	
290 295 300	
tca aaa aca caa agg ccg gaa gag atg cca att tcg aac ctc ggt cgc	1019
Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg	
305 310 315 320	
agg agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg	1067
Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly	
325 330 335	
caa tgg gat ccc cac att gtt gag tgg cac tgaacaa	1104
Gln Trp Asp Pro His Ile Val Glu Trp His	
340 345	
<210> 84	
<211> 346	
<212> PRT	
<213> Homo sapiens	
<400> 84	
Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln	
1 5 10 15	
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly	
20 25 30	
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys	
35 40 45	
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu	

50					55					60					
Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His
65					70					75					80
Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala
				85					90					95	
Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Gly
			100					105					110		
Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	Thr	Ile	Ser
		115					120					125			
Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile
		130				135					140				
Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys	Val	Gln	Glu
145					150					155					160
Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala	Asn	Gly	Trp
				165					170					175	
His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu	Gly	Ile	Ile
			180					185					190		
Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	Arg	Gln	Gln
		195					200					205			
Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val
	210					215					220				
Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg
225					230					235					240
Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val
			245						250					255	
His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met
			260					265					270		
Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe
		275					280					285			
Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln	Pro	Gly	His
	290				295					300					
Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn	Leu	Gly	Arg
305					310					315					320
Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	Gln	Ser	Asp	Gly
				325					330					335	
Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His						
			340					345							

<210> 85

<211> 1104
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(1097)

<400> 85
 gtgccattgt ggggactccc tgggctgctc tgcacccgga cacttgctct gtccccgcc 59

atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac acc atc tcc cag 107
 Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
 1 5 10 15

gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg ggc gca cta gac 155
 Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Asp
 20 25 30

aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag acc tgg aag 203
 Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
 35 40 45

ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat ttc ctc ctt 251
 Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60

atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga cgt aga cac 299
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65 70 75 80

tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc acg ttg gcc 347
 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95

atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg gct gcg ggc 395
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Gly
 100 105 110

agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac act atc tcc 443
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125

acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc ctg gtc atc 491
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140

ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc gtg caa gag 539
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160

acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc aat ggc tgg 587
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175

cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc ggc atc atc 635
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile

180					185					190						
tta	ttt	tgc	tcc	ttc	aag	att	gtt	tgg	agc	ctg	agg	cgg	agg	cag	cag	683
Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	Arg	Gln	Gln	
		195					200					205				
ctg	gcc	aga	cag	gct	cgg	atg	aag	aag	gcg	acc	cgg	ttc	atc	atg	gtg	731
Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val	
	210					215					220					
gtg	gca	att	gtg	ttc	atc	aca	tgc	tac	ctg	ccc	agc	gtg	tct	gct	aga	779
Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg	
225					230					235					240	
ctc	tat	ttc	ctc	tgg	acg	gtg	ccc	tcg	agt	gcc	tgc	gat	ccc	tct	gtc	827
Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val	
			245					250						255		
cat	ggg	gcc	ctg	cac	ata	acc	ctc	agc	ttc	acc	tac	atg	aac	agc	atg	875
His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met	
		260						265					270			
ctg	gat	ccc	ctg	gtg	tat	tat	ttt	tca	agc	ccc	tcc	ttt	ccc	aaa	ttc	923
Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe	
	275						280					285				
tac	aac	aag	ctc	aaa	atc	tgc	agt	ctg	aaa	ccc	aag	cag	cca	gga	cac	971
Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln	Pro	Gly	His	
	290				295					300						
tca	aaa	aca	caa	agg	ccg	gaa	gag	atg	cca	att	tcg	aac	ctc	ggg	cgc	1019
Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn	Leu	Gly	Arg	
305					310					315					320	
agg	agt	tgc	atc	agt	gtg	gca	aat	agt	ttc	caa	agc	cag	tct	gat	ggg	1067
Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	Gln	Ser	Asp	Gly	
			325					330					335			
caa	tgg	gat	ccc	cac	att	gtt	gag	tgg	cac	tga	caa					1104
Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His							
		340					345									
<210> 86																
<211> 346																
<212> PRT																
<213> Homo sapiens																
<400> 86																
Met	Tyr	Asn	Gly	Ser	Cys	Cys	Arg	Ile	Glu	Gly	Asp	Thr	Ile	Ser	Gln	
1				5					10					15		
Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	Gly	Ala	Leu	Asp	
			20					25					30			
Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys	Thr	Trp	Lys	
		35					40					45				

Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
 50 55 60
 Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
 65 70 75 80
 Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Gly
 100 105 110
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 210 215 220
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 225 230 235 240
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
 245 250 255
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
 260 265 270
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
 275 280 285
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
 290 295 300
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
 305 310 315 320
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
 325 330 335
 Gln Trp Asp Pro His Ile Val Glu Trp His
 340 345

<210> 87
 <211> 961
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (11)..(952)

```

<400> 87
caccagatct aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag      49
      Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys
            1              5              10

acc tgg aag ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat      97
Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp
      15              20              25

ttc ctc ctt atg atc tgc ctg cct ttt cgg aca gac tat tac ctc aga      145
Phe Leu Leu Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg
      30              35              40              45

cgt aga cac tgg gct ttt ggg gac att ccc tgc cga gtg ggg ctc ttc      193
Arg Arg His Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe
            50              55              60

acg ttg gcc atg aac agg gcc ggg agc atc gtg ttc ctt acg gtg gtg      241
Thr Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val
            65              70              75

gct gcg gac agg tat ttc aaa gtg gtc cac ccc cac cac gcg gtg aac      289
Ala Ala Asp Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn
            80              85              90

act atc tcc acc cgg gtg gcg gct ggc atc gtc tgc acc ctg tgg gcc      337
Thr Ile Ser Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala
            95              100             105

ctg gtc atc ctg gga aca gtg tat ctt ttg ctg gag aac cat ctc tgc      385
Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys
      110              115              120              125

gtg caa gag acg gcc gtc tcc tgt gag agc ttc atc atg gag tcg gcc      433
Val Gln Glu Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala
            130              135              140

aat ggc tgg cat gac atc atg ttc cag ctg gag ttc ttt atg ccc ctc      481
Asn Gly Trp His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu
            145              150              155

ggc atc atc tta ttt tgc tcc ttc aag att gtt tgg agc ctg agg cgg      529
Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg
            160              165              170

agg cag cag ctg gcc aga cag gct cgg atg aag aag gcg acc cgg ttc      577
Arg Gln Gln Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe
            175              180              185

```

atc atg gtg gtg gca att gtg ttc atc aca tgc tac ctg ccc agc gtg	625
Ile Met Val Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val	
190 195 200 205	
tct gct aga ctc tat ttc ctc tgg acg gtg ccc tcg agt gcc tgc gat	673
Ser Ala Arg Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp	
210 215 220	
ccc tct gtc cat ggg gcc ctg cac ata acc ctc agc ttc acc tac atg	721
Pro Ser Val His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met	
225 230 235	
aac agc atg ctg gat ccc ctg gtg tat tat ttt tca agc ccc tcc ttt	769
Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe	
240 245 250	
ccc aaa ttc tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag	817
Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln	
255 260 265	
cca gga cac tca aaa aca caa agg ccg gaa gag atg cca att tcg aac	865
Pro Gly His Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn	
270 275 280 285	
ctc ggt cgc agg agt tgc atc agt gtg gca aat agt ttc caa agc cag	913
Leu Gly Arg Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln	
290 295 300	
tct gat ggg caa tgg gat ccc cac att gtt gag tgg cac aagcttggc	961
Ser Asp Gly Gln Trp Asp Pro His Ile Val Glu Trp His	
305 310	
<210> 88	
<211> 314	
<212> PRT	
<213> Homo sapiens	
<400> 88	
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys	
1 5 10 15	
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu	
20 25 30	
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His	
35 40 45	
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala	
50 55 60	
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp	
65 70 75 80	
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser	
85 90 95	

Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 100 105 110
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 115 120 125
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 130 135 140
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 145 150 155 160
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 165 170 175
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 180 185 190
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 195 200 205
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
 210 215 220
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
 225 230 235 240
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
 245 250 255
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
 260 265 270
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
 275 280 285
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
 290 295 300
 Gln Trp Asp Pro His Ile Val Glu Trp His
 305 310

<210> 89

<211> 1060

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14) .. (1051)

<400> 89

cacctcgcca acc atg tac aac ggg tcg tgc tgc cgc atc gag ggg gac 49
 Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp
 1 5 10

acc atc tcc cag gtg atg ccg ccg ctg ctc att gtg gcc ttt gtg ctg 97

Thr	Ile	Ser	Gln	Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	
		15					20					25				
ggc	gca	cta	ggc	aat	ggg	gtc	gcc	ctg	tgt	ggg	ttc	tgc	ttc	cac	atg	145
Gly	Ala	Leu	Gly	Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	
	30					35				40						
aag	acc	tgg	aag	ccc	agc	act	gtt	tac	ctt	ttc	aat	ttg	gcc	gtg	gct	193
Lys	Thr	Trp	Lys	Pro	Ser	Thr	Val	Tyr	Leu	Phe	Asn	Leu	Ala	Val	Ala	
45				50					55					60		
gat	ttc	ctc	ctt	atg	atc	tgc	ctg	cct	ttt	cgg	aca	gac	tat	tac	ctc	241
Asp	Phe	Leu	Leu	Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	
				65				70						75		
aga	cgt	aga	cac	tgg	gct	ttt	ggg	gac	att	ccc	tgc	cga	gtg	ggg	ctc	289
Arg	Arg	Arg	His	Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	
			80				85					90				
ttc	acg	ttg	gcc	atg	aac	agg	gcc	ggg	agc	atc	gtg	ttc	ctt	acg	gtg	337
Phe	Thr	Leu	Ala	Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	
	95					100					105					
gtg	gct	gcg	gac	agg	tat	ttc	aaa	gtg	gtc	cac	ccc	cac	cac	gcg	gtg	385
Val	Ala	Ala	Asp	Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	
	110					115				120						
aac	act	atc	tcc	acc	cgg	gtg	gcg	gct	ggc	atc	gtc	tgc	acc	ctg	tgg	433
Asn	Thr	Ile	Ser	Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	
125					130				135					140		
gcc	ctg	gtc	atc	ctg	gga	aca	gtg	tat	ctt	ttg	ctg	gag	aac	cat	ctc	481
Ala	Leu	Val	Ile	Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	
				145				150						155		
tgc	gtg	caa	gag	acg	gcc	gtc	tcc	tgt	gag	agc	ttc	atc	atg	gag	tcg	529
Cys	Val	Gln	Glu	Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	
		160					165					170				
gcc	aat	ggc	tgg	cat	gac	atc	atg	ttc	cag	ctg	gag	ttc	ttt	atg	ccc	577
Ala	Asn	Gly	Trp	His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	
	175					180					185					
ctc	ggc	atc	atc	tta	ttt	tgc	tcc	ttc	aag	att	gtt	tgg	agc	ctg	agg	625
Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	
	190					195				200						
cgg	agg	cag	cag	ctg	gcc	aga	cag	gct	cgg	atg	aag	aag	gcg	acc	cgg	673
Arg	Arg	Gln	Gln	Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	
205				210				215						220		
ttc	atc	atg	gtg	gtg	gca	att	gtg	ttc	atc	aca	tgc	tac	ctg	ccc	agc	721
Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	
				225				230					235			
gtg	tct	gct	aga	ctc	tat	ttc	ctc	tgg	acg	gtg	ccc	tcg	agt	gcc	tgc	769
Val	Ser	Ala	Arg	Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	

240					245					250						
gat	ccc	tct	gtc	cat	ggg	gcc	ctg	cac	ata	acc	ctc	agc	ttc	acc	tac	817
Asp	Pro	Ser	Val	His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	
		255					260					265				
atg	aac	agc	atg	ctg	gat	ccc	ctg	gtg	tat	tat	ttt	tca	agc	ccc	tcc	865
Met	Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	
	270					275					280					
ttt	ccc	aaa	ttc	tac	aac	aag	ctc	aaa	atc	tgc	agt	ctg	aaa	ccc	aag	913
Phe	Pro	Lys	Phe	Tyr	Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	
285					290					295					300	
cag	cca	gga	cac	tca	aaa	aca	caa	agg	ccg	gaa	gag	atg	cca	att	tcg	961
Gln	Pro	Gly	His	Ser	Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	
			305					310					315			
aac	ctc	ggt	cgc	agg	agt	tgc	atc	agt	gtg	gca	aat	agt	ttc	caa	agc	1009
Asn	Leu	Gly	Arg	Arg	Ser	Cys	Ile	Ser	Val	Ala	Asn	Ser	Phe	Gln	Ser	
			320				325					330				
cag	tct	gat	ggg	caa	tgg	gat	ccc	cac	att	gtt	gag	tgg	cac	gtc	gac	1060
Gln	Ser	Asp	Gly	Gln	Trp	Asp	Pro	His	Ile	Val	Glu	Trp	His			
		335					340					345				
<210> 90																
<211> 346																
<212> PRT																
<213> Homo sapiens																
<400> 90																
Met	Tyr	Asn	Gly	Ser	Cys	Cys	Arg	Ile	Glu	Gly	Asp	Thr	Ile	Ser	Gln	
1				5					10					15		
Val	Met	Pro	Pro	Leu	Leu	Ile	Val	Ala	Phe	Val	Leu	Gly	Ala	Leu	Gly	
			20				25						30			
Asn	Gly	Val	Ala	Leu	Cys	Gly	Phe	Cys	Phe	His	Met	Lys	Thr	Trp	Lys	
		35					40					45				
Pro	Ser	Thr	Val	Tyr	Leu	Phe	Asn	Leu	Ala	Val	Ala	Asp	Phe	Leu	Leu	
		50					55					60				
Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	Arg	Arg	His	
65					70				75						80	
Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala	
			85					90						95		
Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Asp	
			100					105					110			
Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	Thr	Ile	Ser	
		115					120					125				
Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile	

130	135	140
Leu Gly Thr Val Tyr	Leu Leu Leu Glu Asn	His Leu Cys Val Gln Glu
145	150	155 160
Thr Ala Val Ser Cys	Glu Ser Phe Ile Met	Glu Ser Ala Asn Gly Trp
	165	170 175
His Asp Ile Met Phe	Gln Leu Glu Phe Phe	Met Pro Leu Gly Ile Ile
	180	185 190
Leu Phe Cys Ser Phe	Lys Ile Val Trp Ser	Leu Arg Arg Arg Gln Gln
	195	200 205
Leu Ala Arg Gln Ala	Arg Met Lys Lys Ala	Thr Arg Phe Ile Met Val
	210	215 220
Val Ala Ile Val Phe	Ile Thr Cys Tyr Leu	Pro Ser Val Ser Ala Arg
	225	230 235 240
Leu Tyr Phe Leu Trp	Thr Val Pro Ser Ser	Ala Cys Asp Pro Ser Val
	245	250 255
His Gly Ala Leu His	Ile Thr Leu Ser Phe	Thr Tyr Met Asn Ser Met
	260	265 270
Leu Asp Pro Leu Val	Tyr Tyr Phe Ser Ser	Pro Ser Phe Pro Lys Phe
	275	280 285
Tyr Asn Lys Leu Lys	Ile Cys Ser Leu Lys	Pro Lys Gln Pro Gly His
	290	295 300
Ser Lys Thr Gln Arg	Pro Glu Glu Met Pro	Ile Ser Asn Leu Gly Arg
	305	310 315 320
Arg Ser Cys Ile Ser	Val Ala Asn Ser Phe	Gln Ser Gln Ser Asp Gly
	325	330 335
Gln Trp Asp Pro His	Ile Val Glu Trp His	
	340	345

<210> 91

<211> 961

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(961)

<400> 91

c acc tcg cga aat ggg gtc gcc ctg tgt ggt ttc tgc ttc cac atg aag	49
Thr Ser Arg Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys	
1 5 10 15	

acc tgg aag ccc agc act gtt tac ctt ttc aat ttg gcc gtg gct gat	97
Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp	

20					25					30						
ttc	ctc	ctt	atg	atc	tgc	ctg	cct	ttt	cgg	aca	gac	tat	tac	ctc	aga	145
Phe	Leu	Leu	Met	Ile	Cys	Leu	Pro	Phe	Arg	Thr	Asp	Tyr	Tyr	Leu	Arg	
35			40			45										
cgt	aga	cac	tgg	gct	ttt	ggg	gac	att	ccc	tgc	cga	gtg	ggg	ctc	ttc	193
Arg	Arg	His	Trp	Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	
50		55		60												
acg	ttg	gcc	atg	aac	agg	gcc	ggg	agc	atc	gtg	ttc	ctt	acg	gtg	gtg	241
Thr	Leu	Ala	Met	Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	
65		70		75		80										
gct	gcg	gac	agg	tat	ttc	aaa	gtg	gtc	cac	ccc	cac	cac	gcg	gtg	aac	289
Ala	Ala	Asp	Arg	Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	
85			90			95										
act	atc	tcc	acc	cgg	gtg	gcg	gct	ggc	atc	gtc	tgc	acc	ctg	tgg	gcc	337
Thr	Ile	Ser	Thr	Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	
100			105			110										
ctg	gtc	atc	ctg	gga	aca	gtg	tat	ctt	ttg	ctg	gag	aac	cat	ctc	tgc	385
Leu	Val	Ile	Leu	Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys	
115		120		125												
gtg	caa	gag	acg	gcc	gtc	tcc	tgt	gag	agc	ttc	atc	atg	gag	tcg	gcc	433
Val	Gln	Glu	Thr	Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala	
130		135		140												
aat	ggc	tgg	cat	gac	atc	atg	ttc	cag	ctg	gag	ttc	ttt	atg	ccc	ctc	481
Asn	Gly	Trp	His	Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu	
145		150		155		160										
ggc	atc	atc	tta	ttt	tgc	tcc	ttc	aag	att	gtt	tgg	agc	ctg	agg	cgg	529
Gly	Ile	Ile	Leu	Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	
165			170			175										
agg	cag	cag	ctg	gcc	aga	cag	gct	cgg	atg	aag	aag	gcg	acc	cgg	ttc	577
Arg	Gln	Gln	Leu	Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	
180			185			190										
atc	atg	gtg	gtg	gca	att	gtg	ttc	atc	aca	tgc	tac	ctg	ccc	agc	gtg	625
Ile	Met	Val	Val	Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	
195		200		205												
tct	gct	aga	ctc	tat	ttc	ctc	tgg	acg	gtg	ccc	tcg	agt	gcc	tgc	gat	673
Ser	Ala	Arg	Leu	Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	
210		215		220												
ccc	tct	gtc	cat	ggg	gcc	ctg	cac	ata	acc	ctc	agc	ttc	acc	tac	atg	721
Pro	Ser	Val	His	Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	
225		230		235		240										
aac	agc	atg	ctg	gat	ccc	ctg	gtg	tat	tat	ttt	tca	agc	ccc	tcc	ttt	769
Asn	Ser	Met	Leu	Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	
245			250			255										

ccc aaa ttc tac aac aag ctc aaa atc tgc agt ctg aaa ccc aag cag 817
 Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln
 260 265 270

cca gga cac tca aaa aca caa agg ccg gaa gag atg cca att tcg aac 865
 Pro Gly His Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn
 275 280 285

ctc ggt cgc agg agt tgc atc agt gtg gca aat agt ttc caa agc cag 913
 Leu Gly Arg Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln
 290 295 300

tct gat ggg caa tgg gat ccc cac att gtt gag tgg cac gtc gac ggc 961
 Ser Asp Gly Gln Trp Asp Pro His Ile Val Glu Trp His Val Asp Gly
 305 310 315 320

<210> 92
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 92
 Thr Ser Arg Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys
 1 5 10 15
 Thr Trp Lys Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp
 20 25 30
 Phe Leu Leu Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg
 35 40 45
 Arg Arg His Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe
 50 55 60
 Thr Leu Ala Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val
 65 70 75 80
 Ala Ala Asp Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn
 85 90 95
 Thr Ile Ser Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala
 100 105 110
 Leu Val Ile Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys
 115 120 125
 Val Gln Glu Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala
 130 135 140
 Asn Gly Trp His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu
 145 150 155 160
 Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg
 165 170 175
 Arg Gln Gln Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe

Ala	Phe	Gly	Asp	Ile	Pro	Cys	Arg	Val	Gly	Leu	Phe	Thr	Leu	Ala	Met		
				85					90					95			
aac	agg	gcc	ggg	agc	atc	gtg	ttc	ctt	acg	gtg	gtg	gct	gcg	gac	agg	336	
Asn	Arg	Ala	Gly	Ser	Ile	Val	Phe	Leu	Thr	Val	Val	Ala	Ala	Asp	Arg		
			100					105					110				
tat	ttc	aaa	gtg	gtc	cac	ccc	cac	cac	gcg	gtg	aac	act	atc	tcc	acc	384	
Tyr	Phe	Lys	Val	Val	His	Pro	His	His	Ala	Val	Asn	Thr	Ile	Ser	Thr		
		115					120					125					
cgg	gtg	gcg	gct	ggc	atc	gtc	tgc	acc	ctg	tgg	gcc	ctg	gtc	atc	ctg	432	
Arg	Val	Ala	Ala	Gly	Ile	Val	Cys	Thr	Leu	Trp	Ala	Leu	Val	Ile	Leu		
	130					135					140						
gga	aca	gtg	tat	ctt	ttg	ctg	gag	aac	cat	ctc	tgc	gtg	caa	gag	acg	480	
Gly	Thr	Val	Tyr	Leu	Leu	Leu	Glu	Asn	His	Leu	Cys	Val	Gln	Glu	Thr		
145					150					155					160		
gcc	gtc	tcc	tgt	gag	agc	ttc	atc	atg	gag	tcg	gcc	aat	ggc	tgg	cat	528	
Ala	Val	Ser	Cys	Glu	Ser	Phe	Ile	Met	Glu	Ser	Ala	Asn	Gly	Trp	His		
				165					170					175			
gac	atc	atg	ttc	cag	ctg	gag	ttc	ttt	atg	ccc	ctc	ggc	atc	atc	tta	576	
Asp	Ile	Met	Phe	Gln	Leu	Glu	Phe	Phe	Met	Pro	Leu	Gly	Ile	Ile	Leu		
			180					185					190				
ttt	tgc	tcc	ttc	aag	att	gtt	tgg	agc	ctg	agg	cgg	agg	cag	cag	ctg	624	
Phe	Cys	Ser	Phe	Lys	Ile	Val	Trp	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Leu		
		195					200					205					
gcc	aga	cag	gct	cgg	atg	aag	aag	gcg	acc	cgg	ttc	atc	atg	gtg	gtg	672	
Ala	Arg	Gln	Ala	Arg	Met	Lys	Lys	Ala	Thr	Arg	Phe	Ile	Met	Val	Val		
	210					215					220						
gca	att	gtg	ttc	atc	aca	tgc	tac	ctg	ccc	agc	gtg	tct	gct	aga	ctc	720	
Ala	Ile	Val	Phe	Ile	Thr	Cys	Tyr	Leu	Pro	Ser	Val	Ser	Ala	Arg	Leu		
225					230					235					240		
tat	ttc	ctc	tgg	acg	gtg	ccc	tcg	agt	gcc	tgc	gat	ccc	tct	gtc	cat	768	
Tyr	Phe	Leu	Trp	Thr	Val	Pro	Ser	Ser	Ala	Cys	Asp	Pro	Ser	Val	His		
				245					250					255			
ggg	gcc	ctg	cac	ata	acc	ctc	agc	ttc	acc	tac	atg	aac	agc	atg	ctg	816	
Gly	Ala	Leu	His	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met	Leu		
			260					265					270				
gat	ccc	ctg	gtg	tat	tat	ttt	tca	agc	ccc	tcc	ttt	ccc	aaa	ttc	tac	864	
Asp	Pro	Leu	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Lys	Phe	Tyr		
		275					280					285					
aac	aag	ctc	aaa	atc	tgc	agt	ctg	aaa	ccc	aag	cag	cca	gga	cac	tca	912	
Asn	Lys	Leu	Lys	Ile	Cys	Ser	Leu	Lys	Pro	Lys	Gln	Pro	Gly	His	Ser		
	290					295					300						
aaa	aca	caa	agg	ccg	gaa	gag	atg	cca	att	tcg	aac	ctc	ggt	cgc	agg	960	
Lys	Thr	Gln	Arg	Pro	Glu	Glu	Met	Pro	Ile	Ser	Asn	Leu	Gly	Arg	Arg		

305	310										315					320					
agt tgc atc agt gtg gca aat agt ttc caa agc cag tct gat ggg caa																					1008
Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly Gln																					
	325										330					335					
tgg gat ccc cac att gtt gag tgg cac gaattcggc																					1044
Trp Asp Pro His Ile Val Glu Trp His																					
	340										345										
<210> 94																					
<211> 345																					
<212> PRT																					
<213> Homo sapiens																					
<400> 94																					
Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln Val																					
1	5										10					15					
Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly Asn																					
	20										25					30					
Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys Pro																					
	35										40					45					
Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met																					
	50										55					60					
Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp																					
65	70										75					80					
Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met																					
	85										90					95					
Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg																					
	100										105					110					
Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr																					
	115										120					125					
Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu																					
	130										135					140					
Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr																					
145	150										155					160					
Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His																					
	165										170					175					
Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu																					
	180										185					190					
Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu																					
	195										200					205					
Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val																					
	210										215					220					

Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu
225 230 235 240

Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His
245 250 255

Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu
260 265 270

Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr
275 280 285

Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser
290 295 300

Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg Arg
305 310 315 320

Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly Gln
325 330 335

Trp Asp Pro His Ile Val Glu Trp His
340 345

<210> 95

<211> 1254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (7) .. (999)

<400> 95

ctaaag atg aaa cgg ctg gtt tgt gtg ctc ttg gtg tgc tcc tct gca 48
Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala
1 5 10

gtg gca cag ttg cat aaa gat cct acc ctg gat cac cac tgg cat ctc 96
Val Ala Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu
15 20 25 30

tgg aag aaa acc tat ggc aaa caa tac aag gaa aag aat gaa gaa gca 144
Trp Lys Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala
35 40 45

gta cga cgt ctc atc tgg gaa aag aat cta aag ttt gtg atg ctt cac 192
Val Arg Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His
50 55 60

aac ctg gag cat tca atg gga atg cac tca tac gat ctg ggc atg aac 240
Asn Leu Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn
65 70 75

cac ctg gga gac atg acc agt gaa gaa gtg atg tct ttg atg agt tcc 288
His Leu Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser

80					85					90										
ctg	aga	gtt	ccc	agc	cag	tgg	cag	aga	aat	atc	aca	tat	aag	tca	aac	336				
Leu	Arg	Val	Pro	Ser	Gln	Trp	Gln	Arg	Asn	Ile	Thr	Tyr	Lys	Ser	Asn					
95					100					105					110					
cct	aat	cgg	ata	ttg	cct	gat	tct	gtg	gac	tgg	aga	gag	aaa	ggg	tgt	384				
Pro	Asn	Arg	Ile	Leu	Pro	Asp	Ser	Val	Asp	Trp	Arg	Glu	Lys	Gly	Cys					
				115					120					125						
gtt	act	gaa	gtg	aaa	tat	caa	ggg	tct	tgt	ggg	gct	tgc	tgg	gct	ttc	432				
Val	Thr	Glu	Val	Lys	Tyr	Gln	Gly	Ser	Cys	Gly	Ala	Cys	Trp	Ala	Phe					
			130					135					140							
agt	gct	gtg	ggg	gcc	ctg	gaa	gca	cag	ctg	aag	ctg	aaa	aca	gga	aag	480				
Ser	Ala	Val	Gly	Ala	Leu	Glu	Ala	Gln	Leu	Lys	Leu	Lys	Thr	Gly	Lys					
		145					150					155								
ctg	gtg	tct	ctc	agt	gcc	cag	aac	ctg	gtg	gat	tgc	tca	act	gaa	aaa	528				
Leu	Val	Ser	Leu	Ser	Ala	Gln	Asn	Leu	Val	Asp	Cys	Ser	Thr	Glu	Lys					
	160					165					170									
tat	gga	aac	aaa	ggc	tgc	aat	ggg	ggc	ttc	atg	aca	acg	gct	ttc	cag	576				
Tyr	Gly	Asn	Lys	Gly	Cys	Asn	Gly	Gly	Phe	Met	Thr	Thr	Ala	Phe	Gln					
175				180					185						190					
tac	atc	att	gat	aac	aag	ggc	atc	gac	tca	gac	gct	tcc	tat	ccc	tac	624				
Tyr	Ile	Ile	Asp	Asn	Lys	Gly	Ile	Asp	Ser	Asp	Ala	Ser	Tyr	Pro	Tyr					
				195					200					205						
aaa	gcc	atg	gat	cag	aaa	tgt	caa	tat	gac	tca	aaa	tat	cgt	gct	gcc	672				
Lys	Ala	Met	Asp	Gln	Lys	Cys	Gln	Tyr	Asp	Ser	Lys	Tyr	Arg	Ala	Ala					
			210					215					220							
aca	tgt	tca	aag	tac	act	gaa	ctt	cct	tat	ggc	aga	gaa	gat	gtc	ctg	720				
Thr	Cys	Ser	Lys	Tyr	Thr	Glu	Leu	Pro	Tyr	Gly	Arg	Glu	Asp	Val	Leu					
		225					230					235								
aaa	gaa	gct	gtg	gcc	aat	aga	ggc	cca	gtg	tct	gtt	ggg	gta	gat	gcg	768				
Lys	Glu	Ala	Val	Ala	Asn	Arg	Gly	Pro	Val	Ser	Val	Gly	Val	Asp	Ala					
	240					245					250									
cgt	cat	cct	tcc	ttc	ttc	ctc	tac	aga	agt	ggg	gtc	tac	tat	gaa	cca	816				
Arg	His	Pro	Ser	Phe	Phe	Leu	Tyr	Arg	Ser	Gly	Val	Tyr	Tyr	Glu	Pro					
255				260						265					270					
tcc	tgt	act	cag	aat	gtg	aat	cat	ggg	gta	ctt	gtg	gtt	ggc	tat	ggg	864				
Ser	Cys	Thr	Gln	Asn	Val	Asn	His	Gly	Val	Leu	Val	Val	Gly	Tyr	Gly					
				275					280					285						
gat	ctt	aat	ggg	aaa	gaa	tac	tgg	ctt	gtg	aaa	aac	agc	tgg	ggg	cac	912				
Asp	Leu	Asn	Gly	Lys	Glu	Tyr	Trp	Leu	Val	Lys	Asn	Ser	Trp	Gly	His					
			290					295					300							
aac	ttt	ggg	gaa	gaa	gga	tat	att	cgg	atg	gca	aga	aat	aaa	gga	aat	960				
Asn	Phe	Gly	Glu	Glu	Gly	Tyr	Ile	Arg	Met	Ala	Arg	Asn	Lys	Gly	Asn					
		305					310					315								

cat tgt ggg att gct agc ttt ccc tct tac cca gaa atc tagaggatct 1009
 His Cys Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile
 320 325 330

ctcctttttaa taacaaatca agaaatatga agcacttttct cttaacttaa tttttcctgc 1069
 tgtatccaga agaaataatt gtgtcatgat taatgtgtat ttactgtact aattagaaaa 1129
 tatagtttga ggccgggcac ggtggctcac gcctgtaatc ccagtacttg ggaggccaag 1189
 gcaggcatat caacttgagg ccaggagtta aagagcagcc tggctaactg tgaaaccctt 1249
 ctact 1254

<210> 96
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala Val Ala
 1 5 10 15
 Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu Trp Lys
 20 25 30
 Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala Val Arg
 35 40 45
 Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His Asn Leu
 50 55 60
 Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn His Leu
 65 70 75 80
 Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser Leu Arg
 85 90 95
 Val Pro Ser Gln Trp Gln Arg Asn Ile Thr Tyr Lys Ser Asn Pro Asn
 100 105 110
 Arg Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val Thr
 115 120 125
 Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser Ala
 130 135 140
 Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu Val
 145 150 155 160
 Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr Gly
 165 170 175
 Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr Ile
 180 185 190

cat tgt ggg att gct agc ttt ccc tct tac cca gaa atc tagaggatct 1009
 His Cys Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile
 320 325 330

ctccttttta taacaaatca agaaatatga agcactttct cttaacttaa tttttcctgc 1069
 tgtatccaga agaaataatt gtgtcatgat taatgtgtat ttactgtact aattagaaaa 1129
 tatagtttga ggccgggcac ggtggctcac gcctgtaatc ccagtacttg ggaggccaag 1189
 gcaggcatat caacttgagg ccaggagtta aagagcagcc tggctaactg tgaaaccct 1249
 ctact 1254

<210> 96
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala Val Ala
 1 5 10 15
 Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu Trp Lys
 20 25 30
 Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala Val Arg
 35 40 45
 Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His Asn Leu
 50 55 60
 Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn His Leu
 65 70 75 80
 Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser Leu Arg
 85 90 95
 Val Pro Ser Gln Trp Gln Arg Asn Ile Thr Tyr Lys Ser Asn Pro Asn
 100 105 110
 Arg Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val Thr
 115 120 125
 Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser Ala
 130 135 140
 Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu Val
 145 150 155 160
 Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr Gly
 165 170 175
 Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr Ile
 180 185 190

Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys Ala
195 200 205

Met Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr Cys
210 215 220

Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys Glu
225 230 235 240

Ala Val Ala Asn Arg Gly Pro Val Ser Val Gly Val Asp Ala Arg His
245 250 255

Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser Cys
260 265 270

Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp Leu
275 280 285

Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn Phe
290 295 300

Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His Cys
305 310 315 320

Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile
325 330

<210> 97
<211> 667
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(667)

<400> 97
c acc aag ctt ttg cct gat tct gtg gac tgg aga gag aaa ggg tgt gtt 49
Thr Lys Leu Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val
1 5 10 15

act gaa gtg aaa tat caa ggt tct tgt ggt gct tgc tgg gct ttc agt 97
Thr Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser
20 25 30

gct gtg ggg gcc ctg gaa gca cag ctg aag ctg aaa aca gga aag ctg 145
Ala Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu
35 40 45

gtg tct ctc agt gcc cag aac ctg gtg gat tgc tca act gaa aaa tat 193
Val Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr
50 55 60

gga aac aaa ggc tgc aat ggt ggc ttc atg aca acg gct ttc cag tac 241
Gly Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr
65 70 75 80

atc att gat aac aag ggc atc gac tca gac gct tcc tat ccc tac aaa	289
Ile Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys	
85 90 95	
gcc atg gat cag aaa tgt caa tat gac tca aaa tat cgt gct gcc aca	337
Ala Met Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr	
100 105 110	
tgt tca aag tac act gaa ctt cct tat ggc aga gaa gat gtc ctg aaa	385
Cys Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys	
115 120 125	
gaa gct gtg gcc aat aga ggc cca gtg tct gtt ggt gta gat gcg cgt	433
Glu Ala Val Ala Asn Arg Gly Pro Val Ser Val Gly Val Asp Ala Arg	
130 135 140	
cat cct tcc ttc ttc ctc tac aga agt ggt gtc tac tat gaa cca tcc	481
His Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser	
145 150 155 160	
tgt act cag aat gtg aat cat ggt gta ctt gtg gtt ggc tat ggt gat	529
Cys Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp	
165 170 175	
ctt aat ggg aaa gaa tac tgg ctt gtg aaa aac agc tgg ggt cac aac	577
Leu Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn	
180 185 190	
ttt ggt gaa gaa gga tat att cgg atg gca aga aat aaa gga aat cat	625
Phe Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His	
195 200 205	
tgt ggg att gct agc ttt ccc tct tac cca gaa gtc gac ggc	667
Cys Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Val Asp Gly	
210 215 220	
<210> 98	
<211> 222	
<212> PRT	
<213> Homo sapiens	
<400> 98	
Thr Lys Leu Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val	
1 5 10 15	
Thr Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser	
20 25 30	
Ala Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu	
35 40 45	
Val Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr	
50 55 60	
Gly Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr	
65 70 75 80	

Ile Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys
 85 90 95
 Ala Met Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr
 100 105 110
 Cys Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys
 115 120 125
 Glu Ala Val Ala Asn Arg Gly Pro Val Ser Val Gly Val Asp Ala Arg
 130 135 140
 His Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser
 145 150 155 160
 Cys Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp
 165 170 175
 Leu Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn
 180 185 190
 Phe Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His
 195 200 205
 Cys Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Val Asp Gly
 210 215 220

<210> 99

<211> 1222

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1155)

<400> 99

attgcggggcg gcggcgttcg gagtcgccgg gagctgccag gctgtccgcg ccgccgctgc 60

ggggcc atg atc cgg aac ggg cgc ggg gct gca ggc ggc gca gag cag 108
 Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala Glu Gln
 1 5 10

ccg ggc ccg ggg ggc agg cgc gcc gtg agg gtg tgg tgc gat ggc tgc 156
 Pro Gly Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp Gly Cys
 15 20 25 30

tat gac atg gtg cat tac ggc cac tcc aac cag ctg cgc cag gca cgg 204
 Tyr Asp Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln Ala Arg
 35 40 45

gcc atg ggt gac tac ctc atc gta ggc gtg cac acc gat gag gag atc 252
 Ala Met Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu Glu Ile
 50 55 60

gcc aag cac aag ggg ccc ccg gtg ttc act cag gag gag aga tac aag 300
 Ala Lys His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg Tyr Lys

65						70						75						
atg	gtg	cag	gcc	atc	aaa	tgg	gtg	gac	gag	gtg	gtg	cca	gcg	gct	ccc	348		
Met	Val	Gln	Ala	Ile	Lys	Trp	Val	Asp	Glu	Val	Val	Pro	Ala	Ala	Pro			
	80						85					90						
tac	gtc	act	aca	cta	gag	acc	ctg	gac	aaa	tac	aac	tgt	gac	ttc	tgt	396		
Tyr	Val	Thr	Thr	Leu	Glu	Thr	Leu	Asp	Lys	Tyr	Asn	Cys	Asp	Phe	Cys			
	95				100					105					110			
gtt	cac	ggc	aat	gac	atc	acc	ctg	act	gta	gat	ggc	cgg	gac	acc	tat	444		
Val	His	Gly	Asn	Asp	Ile	Thr	Leu	Thr	Val	Asp	Gly	Arg	Asp	Thr	Tyr			
				115					120					125				
gag	gaa	gta	aag	cag	gct	ggg	agg	tac	aga	gaa	tgc	aag	cgc	acg	caa	492		
Glu	Glu	Val	Lys	Gln	Ala	Gly	Arg	Tyr	Arg	Glu	Cys	Lys	Arg	Thr	Gln			
			130					135					140					
ggg	gtg	tcc	acc	aca	gac	ctc	gtg	ggc	cgc	atg	ctg	ctg	gta	acc	aaa	540		
Gly	Val	Ser	Thr	Thr	Asp	Leu	Val	Gly	Arg	Met	Leu	Leu	Val	Thr	Lys			
		145					150					155						
gcc	cat	cac	agc	agc	cag	gag	atg	tcc	tct	gag	tac	cgg	gag	tat	gca	588		
Ala	His	His	Ser	Ser	Gln	Glu	Met	Ser	Ser	Glu	Tyr	Arg	Glu	Tyr	Ala			
	160					165				170								
gac	agt	ttt	ggc	aag	tgc	cct	ggg	ggg	cgg	aac	ccc	tgg	acc	ggg	gta	636		
Asp	Ser	Phe	Gly	Lys	Cys	Pro	Gly	Gly	Arg	Asn	Pro	Trp	Thr	Gly	Val			
	175				180					185					190			
tcc	cag	ttc	ctg	cag	aca	tct	cag	aag	atc	atc	cag	ttt	gct	tct	ggg	684		
Ser	Gln	Phe	Leu	Gln	Thr	Ser	Gln	Lys	Ile	Ile	Gln	Phe	Ala	Ser	Gly			
				195					200					205				
aag	gag	ccc	cag	cca	ggg	gag	aca	gtc	atc	tat	gtg	gct	ggg	gcc	ttc	732		
Lys	Glu	Pro	Gln	Pro	Gly	Glu	Thr	Val	Ile	Tyr	Val	Ala	Gly	Ala	Phe			
			210					215					220					
gac	ctg	ttc	cac	atc	ggg	cat	gtg	gac	ttc	ctg	gag	aag	gtg	cac	agg	780		
Asp	Leu	Phe	His	Ile	Gly	His	Val	Asp	Phe	Leu	Glu	Lys	Val	His	Arg			
		225					230					235						
ctg	gca	gag	agg	ccc	tac	atc	atc	gcg	ggc	tta	cac	ttt	gac	cag	tac	828		
Leu	Ala	Glu	Arg	Pro	Tyr	Ile	Ile	Ala	Gly	Leu	His	Phe	Asp	Gln	Tyr			
	240					245					250							
gtg	tca	gaa	gtg	gtg	att	gga	gcc	ccg	tac	gcg	gtc	aca	gca	gag	ctc	876		
Val	Ser	Glu	Val	Val	Ile	Gly	Ala	Pro	Tyr	Ala	Val	Thr	Ala	Glu	Leu			
	255				260					265					270			
cta	agt	cac	ttc	aag	gtg	gac	ctg	gtg	tgt	cac	ggc	aag	aca	gga	att	924		
Leu	Ser	His	Phe	Lys	Val	Asp	Leu	Val	Cys	His	Gly	Lys	Thr	Gly	Ile			
				275					280					285				
atc	cct	gac	agg	gat	ggc	tcc	gac	cca	tac	cag	gag	ccc	aag	aga	agg	972		
Ile	Pro	Asp	Arg	Asp	Gly	Ser	Asp	Pro	Tyr	Gln	Glu	Pro	Lys	Arg	Arg			
			290					295					300					

ggc atc ttc cgt cag att gac agt ggc agc aac ctc acc aca gac ctc 1020
 Gly Ile Phe Arg Gln Ile Asp Ser Gly Ser Asn Leu Thr Thr Asp Leu
 305 310 315

atc gtc cag cgg atc atc acc aac agg ttg gag tat gag gcg cga aac 1068
 Ile Val Gln Arg Ile Ile Thr Asn Arg Leu Glu Tyr Glu Ala Arg Asn
 320 325 330

cag aag aag gaa gcc aag gag ctg gcc ttc ctg gag gct gcc agg cag 1116
 Gln Lys Lys Glu Ala Lys Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln
 335 340 345 350

cag gcg gca cag ccc ctg ggg gag cgc gat ggt gac ttc taacctggca 1165
 Gln Ala Ala Gln Pro Leu Gly Glu Arg Asp Gly Asp Phe
 355 360

gagggcctgg ccggccctcc ccctgctctg cttctgcgcc ttctgcgttt ggacata 1222

<210> 100
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala Glu Gln Pro Gly
 1 5 10 15

Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp Gly Cys Tyr Asp
 20 25 30

Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln Ala Arg Ala Met
 35 40 45

Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu Glu Ile Ala Lys
 50 55 60

His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg Tyr Lys Met Val
 65 70 75 80

Gln Ala Ile Lys Trp Val Asp Glu Val Val Pro Ala Ala Pro Tyr Val
 85 90 95

Thr Thr Leu Glu Thr Leu Asp Lys Tyr Asn Cys Asp Phe Cys Val His
 100 105 110

Gly Asn Asp Ile Thr Leu Thr Val Asp Gly Arg Asp Thr Tyr Glu Glu
 115 120 125

Val Lys Gln Ala Gly Arg Tyr Arg Glu Cys Lys Arg Thr Gln Gly Val
 130 135 140

Ser Thr Thr Asp Leu Val Gly Arg Met Leu Leu Val Thr Lys Ala His
 145 150 155 160

His Ser Ser Gln Glu Met Ser Ser Glu Tyr Arg Glu Tyr Ala Asp Ser
 165 170 175

Phe Gly Lys Cys Pro Gly Gly Arg Asn Pro Trp Thr Gly Val Ser Gln
 180 185 190
 Phe Leu Gln Thr Ser Gln Lys Ile Ile Gln Phe Ala Ser Gly Lys Glu
 195 200 205
 Pro Gln Pro Gly Glu Thr Val Ile Tyr Val Ala Gly Ala Phe Asp Leu
 210 215 220
 Phe His Ile Gly His Val Asp Phe Leu Glu Lys Val His Arg Leu Ala
 225 230 235 240
 Glu Arg Pro Tyr Ile Ile Ala Gly Leu His Phe Asp Gln Tyr Val Ser
 245 250 255
 Glu Val Val Ile Gly Ala Pro Tyr Ala Val Thr Ala Glu Leu Leu Ser
 260 265 270
 His Phe Lys Val Asp Leu Val Cys His Gly Lys Thr Gly Ile Ile Pro
 275 280 285
 Asp Arg Asp Gly Ser Asp Pro Tyr Gln Glu Pro Lys Arg Arg Gly Ile
 290 295 300
 Phe Arg Gln Ile Asp Ser Gly Ser Asn Leu Thr Thr Asp Leu Ile Val
 305 310 315 320
 Gln Arg Ile Ile Thr Asn Arg Leu Glu Tyr Glu Ala Arg Asn Gln Lys
 325 330 335
 Lys Glu Ala Lys Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala
 340 345 350
 Ala Gln Pro Leu Gly Glu Arg Asp Gly Asp Phe
 355 360

<210> 101
 <211> 1243
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(1243)

<400> 101
 c acc gga tcc acc atg atc cgg aac ggg cgc ggg gct gca ggc ggc gca 49
 Thr Gly Ser Thr Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala
 1 5 10 15
 gag cag ccg ggc ccg ggg ggc agg cgc gcc gtg agg gtg tgg tgc gat 97
 Glu Gln Pro Gly Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp
 20 25 30
 ggc tgc tat gac atg gtg cat tac ggc cac tcc aac cag ctg cgc cag 145
 Gly Cys Tyr Asp Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln

35					40					45									
gca	cgg	gcc	atg	ggg	gac	tac	ctc	atc	gta	ggc	gtg	cac	acc	gat	gag	193			
Ala	Arg	Ala	Met	Gly	Asp	Tyr	Leu	Ile	Val	Gly	Val	His	Thr	Asp	Glu				
50					55					60									
gag	atc	gcc	aag	cac	aag	ggg	ccc	ccg	gtg	ttc	act	cag	gag	gag	aga	241			
Glu	Ile	Ala	Lys	His	Lys	Gly	Pro	Pro	Val	Phe	Thr	Gln	Glu	Glu	Arg				
65					70					75					80				
tac	aag	atg	gtg	cag	gcc	atc	aaa	tgg	gtg	gac	gag	gtg	gtg	cca	gcg	289			
Tyr	Lys	Met	Val	Gln	Ala	Ile	Lys	Trp	Val	Asp	Glu	Val	Val	Pro	Ala				
85					90					95									
gct	ccc	tac	gtc	act	aca	cta	gag	acc	ctg	gac	aaa	tac	aac	tgt	gac	337			
Ala	Pro	Tyr	Val	Thr	Thr	Leu	Glu	Thr	Leu	Asp	Lys	Tyr	Asn	Cys	Asp				
100					105					110									
ttc	tgt	gtt	cac	ggc	aat	gac	atc	acc	ctg	act	gta	gat	ggc	cgg	gac	385			
Phe	Cys	Val	His	Gly	Asn	Asp	Ile	Thr	Leu	Thr	Val	Asp	Gly	Arg	Asp				
115					120					125									
acc	tat	gag	gaa	gta	aag	cag	gct	ggg	agg	tac	aga	gaa	tgc	aag	cgc	433			
Thr	Tyr	Glu	Glu	Val	Lys	Gln	Ala	Gly	Arg	Tyr	Arg	Glu	Cys	Lys	Arg				
130					135					140									
acg	caa	ggg	gtg	tcc	acc	aca	gac	ctc	gtg	ggc	cgc	atg	ctg	ctg	gta	481			
Thr	Gln	Gly	Val	Ser	Thr	Thr	Asp	Leu	Val	Gly	Arg	Met	Leu	Leu	Val				
145					150					155					160				
acc	aaa	gcc	cat	cac	agc	agc	cag	gag	atg	tcc	tct	gag	tac	cgg	gag	529			
Thr	Lys	Ala	His	His	Ser	Ser	Gln	Glu	Met	Ser	Ser	Glu	Tyr	Arg	Glu				
165					170					175									
tat	gca	gac	agt	ttt	ggc	aag	ccc	cct	cac	ccg	ata	ccc	gcc	ggg	gac	577			
Tyr	Ala	Asp	Ser	Phe	Gly	Lys	Pro	Pro	His	Pro	Ile	Pro	Ala	Gly	Asp				
180					185					190									
ata	ctt	tcc	tca	gaa	ggc	tgc	tcc	cag	tgc	cct	ggg	ggg	cgg	aac	ccc	625			
Ile	Leu	Ser	Ser	Glu	Gly	Cys	Ser	Gln	Cys	Pro	Gly	Gly	Arg	Asn	Pro				
195					200					205									
tgg	acc	ggg	gta	tcc	cag	ttc	ctg	cag	aca	tct	cag	aag	atc	atc	cag	673			
Trp	Thr	Gly	Val	Ser	Gln	Phe	Leu	Gln	Thr	Ser	Gln	Lys	Ile	Ile	Gln				
210					215					220									
ttt	gct	tct	ggg	aag	gag	ccc	cag	cca	ggg	gag	aca	gtc	atc	tat	gtg	721			
Phe	Ala	Ser	Gly	Lys	Glu	Pro	Gln	Pro	Gly	Glu	Thr	Val	Ile	Tyr	Val				
225					230					235					240				
gct	ggg	gcc	ttc	gac	ctg	ttc	cac	atc	ggg	cat	gtg	gac	ttc	ctg	gag	769			
Ala	Gly	Ala	Phe	Asp	Leu	Phe	His	Ile	Gly	His	Val	Asp	Phe	Leu	Glu				
245					250					255									
aag	gtg	cac	agg	ctg	gca	gag	agg	ccc	tac	atc	atc	gcg	ggc	tta	cac	817			
Lys	Val	His	Arg	Leu	Ala	Glu	Arg	Pro	Tyr	Ile	Ile	Ala	Gly	Leu	His				
260					265					270									

ttt gac cag gag gtc aat cac tac aag ggg aag aac tac ccc atc atg	865
Phe Asp Gln Glu Val Asn His Tyr Lys Gly Lys Asn Tyr Pro Ile Met	
275 280 285	
aat ctg cat gaa cgg act ctg agc gtg ctg gcc tgc cgg tac gtg tca	913
Asn Leu His Glu Arg Thr Leu Ser Val Leu Ala Cys Arg Tyr Val Ser	
290 295 300	
gaa gtg gtg att gga gcc ccg tac gcg gtc aca gca gag ctc cta agt	961
Glu Val Val Ile Gly Ala Pro Tyr Ala Val Thr Ala Glu Leu Leu Ser	
305 310 315 320	
cac ttc aag gtg gac ctg gtg tgt cac ggc aag aca gaa att atc cct	1009
His Phe Lys Val Asp Leu Val Cys His Gly Lys Thr Glu Ile Ile Pro	
325 330 335	
gac agg gat ggc tcc gac cca tac cag gag ccc aag aga agg ggc atc	1057
Asp Arg Asp Gly Ser Asp Pro Tyr Gln Glu Pro Lys Arg Arg Gly Ile	
340 345 350	
ttc cgt cag att gac agt ggc agc aac ctc acc aca gac ctc atc gtc	1105
Phe Arg Gln Ile Asp Ser Gly Ser Asn Leu Thr Thr Asp Leu Ile Val	
355 360 365	
cag cgg atc atc acc aac agg ttg gag tat gag gcg cga aac cag aag	1153
Gln Arg Ile Ile Thr Asn Arg Leu Glu Tyr Glu Ala Arg Asn Gln Lys	
370 375 380	
aag gaa gcc aag gag ctg gcc ttc ctg gag gct gcc agg cag cag gcg	1201
Lys Glu Ala Lys Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala	
385 390 395 400	
gca cag ccc ctg ggg gag cgc gat ggt gac ttc ctc gag ggc	1243
Ala Gln Pro Leu Gly Glu Arg Asp Gly Asp Phe Leu Glu Gly	
405 410	
<210> 102	
<211> 414	
<212> PRT	
<213> Homo sapiens	
<400> 102	
Thr Gly Ser Thr Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala	
1 5 10 15	
Glu Gln Pro Gly Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp	
20 25 30	
Gly Cys Tyr Asp Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln	
35 40 45	
Ala Arg Ala Met Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu	
50 55 60	
Glu Ile Ala Lys His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg	
65 70 75 80	

Tyr	Lys	Met	Val	Gln	Ala	Ile	Lys	Trp	Val	Asp	Glu	Val	Val	Pro	Ala	
				85					90					95		
Ala	Pro	Tyr	Val	Thr	Thr	Leu	Glu	Thr	Leu	Asp	Lys	Tyr	Asn	Cys	Asp	
			100					105					110			
Phe	Cys	Val	His	Gly	Asn	Asp	Ile	Thr	Leu	Thr	Val	Asp	Gly	Arg	Asp	
		115					120					125				
Thr	Tyr	Glu	Glu	Val	Lys	Gln	Ala	Gly	Arg	Tyr	Arg	Glu	Cys	Lys	Arg	
	130					135					140					
Thr	Gln	Gly	Val	Ser	Thr	Thr	Asp	Leu	Val	Gly	Arg	Met	Leu	Leu	Val	
145					150					155					160	
Thr	Lys	Ala	His	His	Ser	Ser	Gln	Glu	Met	Ser	Ser	Glu	Tyr	Arg	Glu	
			165						170					175		
Tyr	Ala	Asp	Ser	Phe	Gly	Lys	Pro	Pro	His	Pro	Ile	Pro	Ala	Gly	Asp	
			180					185					190			
Ile	Leu	Ser	Ser	Glu	Gly	Cys	Ser	Gln	Cys	Pro	Gly	Gly	Arg	Asn	Pro	
	195						200					205				
Trp	Thr	Gly	Val	Ser	Gln	Phe	Leu	Gln	Thr	Ser	Gln	Lys	Ile	Ile	Gln	
	210					215					220					
Phe	Ala	Ser	Gly	Lys	Glu	Pro	Gln	Pro	Gly	Glu	Thr	Val	Ile	Tyr	Val	
225					230					235					240	
Ala	Gly	Ala	Phe	Asp	Leu	Phe	His	Ile	Gly	His	Val	Asp	Phe	Leu	Glu	
			245						250					255		
Lys	Val	His	Arg	Leu	Ala	Glu	Arg	Pro	Tyr	Ile	Ile	Ala	Gly	Leu	His	
		260						265					270			
Phe	Asp	Gln	Glu	Val	Asn	His	Tyr	Lys	Gly	Lys	Asn	Tyr	Pro	Ile	Met	
	275						280					285				
Asn	Leu	His	Glu	Arg	Thr	Leu	Ser	Val	Leu	Ala	Cys	Arg	Tyr	Val	Ser	
	290					295					300					
Glu	Val	Val	Ile	Gly	Ala	Pro	Tyr	Ala	Val	Thr	Ala	Glu	Leu	Leu	Ser	
305					310					315					320	
His	Phe	Lys	Val	Asp	Leu	Val	Cys	His	Gly	Lys	Thr	Glu	Ile	Ile	Pro	
			325						330					335		
Asp	Arg	Asp	Gly	Ser	Asp	Pro	Tyr	Gln	Glu	Pro	Lys	Arg	Arg	Gly	Ile	
		340						345					350			
Phe	Arg	Gln	Ile	Asp	Ser	Gly	Ser	Asn	Leu	Thr	Thr	Asp	Leu	Ile	Val	
		355					360					365				
Gln	Arg	Ile	Ile	Thr	Asn	Arg	Leu	Glu	Tyr	Glu	Ala	Arg	Asn	Gln	Lys	
	370					375					380					

Lys Glu Ala Lys Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala
 385 390 395 400

Ala Gln Pro Leu Gly Glu Arg Asp Gly Asp Phe Leu Glu Gly
 405 410

<210> 103
 <211> 1237
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)..(1234)

<400> 103
 caccggatcc acc atg atc cgg aac ggg cgc ggg gct gca ggc ggc gca 49
 Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala
 1 5 10

gag cag ccg ggc ccg ggg ggc agg cgc gcc gtg agg gtg tgg tgc gat 97
 Glu Gln Pro Gly Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp
 15 20 25

ggc tgc tat gac atg gtg cat tac ggc cac tcc aac cag ctg cgc cag 145
 Gly Cys Tyr Asp Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln
 30 35 40

gca cgg gcc atg ggt gac tac ctc atc gta ggc gtg cac acc gat gag 193
 Ala Arg Ala Met Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu
 45 50 55 60

gag atc gcc aag cac aag ggg ccc ccg gtg ttc act cag gag gag aga 241
 Glu Ile Ala Lys His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg
 65 70 75

tac aag atg gtg cag gcc atc aaa tgg gtg gac gag gtg gtg cca gcg 289
 Tyr Lys Met Val Gln Ala Ile Lys Trp Val Asp Glu Val Val Pro Ala
 80 85 90

gct ccc tac gtc act aca cta gag acc ctg gac aaa tac aac tgt gac 337
 Ala Pro Tyr Val Thr Thr Leu Glu Thr Leu Asp Lys Tyr Asn Cys Asp
 95 100 105

ttc tgt gtt cac ggc aat gac atc acc ctg act gta gat ggc cgg gac 385
 Phe Cys Val His Gly Asn Asp Ile Thr Leu Thr Val Asp Gly Arg Asp
 110 115 120

acc tat gag gaa gta aag cag gct ggg agg tac aga gaa tgc aag cgc 433
 Thr Tyr Glu Glu Val Lys Gln Ala Gly Arg Tyr Arg Glu Cys Lys Arg
 125 130 135 140

acg caa ggg gtg tcc acc aca gac ctc gtg ggc cgc atg ctg ctg gta 481
 Thr Gln Gly Val Ser Thr Thr Asp Leu Val Gly Arg Met Leu Leu Val
 145 150 155

acc	aaa	gcc	cat	cac	agc	agc	cag	gag	atg	tcc	tct	gag	tac	cgg	gag	529
Thr	Lys	Ala	His	His	Ser	Ser	Gln	Glu	Met	Ser	Ser	Glu	Tyr	Arg	Glu	
			160					165					170			
tat	gca	gac	agt	ttt	ggc	aag	ccc	cct	cac	ccg	ata	ccc	gcc	ggg	gac	577
Tyr	Ala	Asp	Ser	Phe	Gly	Lys	Pro	Pro	His	Pro	Ile	Pro	Ala	Gly	Asp	
			175				180					185				
ata	ctt	tcc	tca	gaa	ggc	tgc	tcc	cag	tgc	cct	ggg	ggg	cgg	aac	ccc	625
Ile	Leu	Ser	Ser	Glu	Gly	Cys	Ser	Gln	Cys	Pro	Gly	Gly	Arg	Asn	Pro	
	190					195					200					
tgg	acc	ggg	gta	tcc	cag	ttc	ctg	cag	aca	tct	cag	aag	atc	atc	cag	673
Trp	Thr	Gly	Val	Ser	Gln	Phe	Leu	Gln	Thr	Ser	Gln	Lys	Ile	Ile	Gln	
205					210				215						220	
ttt	gct	tct	ggg	aag	gag	ccc	cag	cca	ggg	gag	aca	gtc	atc	tat	gtg	721
Phe	Ala	Ser	Gly	Lys	Glu	Pro	Gln	Pro	Gly	Glu	Thr	Val	Ile	Tyr	Val	
				225					230					235		
gct	ggg	gcc	ttc	gac	ctg	ttc	cac	atc	ggg	cat	gtg	gac	ttc	ctg	gag	769
Ala	Gly	Ala	Phe	Asp	Leu	Phe	His	Ile	Gly	His	Val	Asp	Phe	Leu	Glu	
			240					245					250			
aag	gtg	cac	agg	ctg	gca	gag	agg	ccc	tac	atc	atc	gcg	ggc	tta	cac	817
Lys	Val	His	Arg	Leu	Ala	Glu	Arg	Pro	Tyr	Ile	Ile	Ala	Gly	Leu	His	
			255				260					265				
ttt	gac	cag	gag	gtc	aat	cac	tac	aag	ggg	aag	aac	tac	ccc	atc	atg	865
Phe	Asp	Gln	Glu	Val	Asn	His	Tyr	Lys	Gly	Lys	Asn	Tyr	Pro	Ile	Met	
	270					275					280					
aat	ctg	cat	gaa	cgg	act	ctg	agc	gtg	ctg	gcc	tgc	cgg	tac	gtg	tca	913
Asn	Leu	His	Glu	Arg	Thr	Leu	Ser	Val	Leu	Ala	Cys	Arg	Tyr	Val	Ser	
285					290					295					300	
gaa	gtg	gtg	att	gga	gcc	ccg	tac	gcg	gtc	aca	gca	gag	ctc	cta	agt	961
Glu	Val	Val	Ile	Gly	Ala	Pro	Tyr	Ala	Val	Thr	Ala	Glu	Leu	Leu	Ser	
				305					310					315		
cac	ttc	aag	gtg	gac	ctg	gtg	tgt	cac	ggc	aag	aca	gaa	att	atc	cct	1009
His	Phe	Lys	Val	Asp	Leu	Val	Cys	His	Gly	Lys	Thr	Glu	Ile	Ile	Pro	
			320					325					330			
gac	agg	gat	ggc	tcc	gac	cca	tac	cag	gag	ccc	aag	aga	agg	ggc	atc	1057
Asp	Arg	Asp	Gly	Ser	Asp	Pro	Tyr	Gln	Glu	Pro	Lys	Arg	Arg	Gly	Ile	
			335				340					345				
ttc	cgt	cag	att	gac	agt	ggc	agc	aac	ctc	acc	aca	gac	ctc	atc	gtc	1105
Phe	Arg	Gln	Ile	Asp	Ser	Gly	Ser	Asn	Leu	Thr	Thr	Asp	Leu	Ile	Val	
	350					355					360					
cag	cgg	atc	atc	acc	aac	agg	ttg	gag	tat	gag	gcg	cga	aac	cag	aag	1153
Gln	Arg	Ile	Ile	Thr	Asn	Arg	Leu	Glu	Tyr	Glu	Ala	Arg	Asn	Gln	Lys	
365					370					375					380	
aag	gaa	gcc	aag	gag	ctg	gcc	ttc	ctg	gag	gct	gcc	agg	cag	cag	gcg	1201

Lys Glu Ala Lys Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala
 385 390 395
 gca cag ccc ctg ggg gag cgc gat ggt gac ttc taa 1237
 Ala Gln Pro Leu Gly Glu Arg Asp Gly Asp Phe
 400 405
 <210> 104
 <211> 407
 <212> PRT
 <213> Homo sapiens
 <400> 104
 Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala Glu Gln Pro Gly
 1 5 10 15
 Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp Gly Cys Tyr Asp
 20 25 30
 Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln Ala Arg Ala Met
 35 40 45
 Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu Glu Ile Ala Lys
 50 55 60
 His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg Tyr Lys Met Val
 65 70 75 80
 Gln Ala Ile Lys Trp Val Asp Glu Val Val Pro Ala Ala Pro Tyr Val
 85 90 95
 Thr Thr Leu Glu Thr Leu Asp Lys Tyr Asn Cys Asp Phe Cys Val His
 100 105 110
 Gly Asn Asp Ile Thr Leu Thr Val Asp Gly Arg Asp Thr Tyr Glu Glu
 115 120 125
 Val Lys Gln Ala Gly Arg Tyr Arg Glu Cys Lys Arg Thr Gln Gly Val
 130 135 140
 Ser Thr Thr Asp Leu Val Gly Arg Met Leu Leu Val Thr Lys Ala His
 145 150 155 160
 His Ser Ser Gln Glu Met Ser Ser Glu Tyr Arg Glu Tyr Ala Asp Ser
 165 170 175
 Phe Gly Lys Pro Pro His Pro Ile Pro Ala Gly Asp Ile Leu Ser Ser
 180 185 190
 Glu Gly Cys Ser Gln Cys Pro Gly Gly Arg Asn Pro Trp Thr Gly Val
 195 200 205
 Ser Gln Phe Leu Gln Thr Ser Gln Lys Ile Ile Gln Phe Ala Ser Gly
 210 215 220
 Lys Glu Pro Gln Pro Gly Glu Thr Val Ile Tyr Val Ala Gly Ala Phe
 225 230 235 240

Asp Leu Phe His Ile Gly His Val Asp Phe Leu Glu Lys Val His Arg
 245 250 255
 Leu Ala Glu Arg Pro Tyr Ile Ile Ala Gly Leu His Phe Asp Gln Glu
 260 265 270
 Val Asn His Tyr Lys Gly Lys Asn Tyr Pro Ile Met Asn Leu His Glu
 275 280 285
 Arg Thr Leu Ser Val Leu Ala Cys Arg Tyr Val Ser Glu Val Val Ile
 290 295 300
 Gly Ala Pro Tyr Ala Val Thr Ala Glu Leu Leu Ser His Phe Lys Val
 305 310 315 320
 Asp Leu Val Cys His Gly Lys Thr Glu Ile Ile Pro Asp Arg Asp Gly
 325 330 335
 Ser Asp Pro Tyr Gln Glu Pro Lys Arg Arg Gly Ile Phe Arg Gln Ile
 340 345 350
 Asp Ser Gly Ser Asn Leu Thr Thr Asp Leu Ile Val Gln Arg Ile Ile
 355 360 365
 Thr Asn Arg Leu Glu Tyr Glu Ala Arg Asn Gln Lys Lys Glu Ala Lys
 370 375 380
 Glu Leu Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala Ala Gln Pro Leu
 385 390 395 400
 Gly Glu Arg Asp Gly Asp Phe
 405

<210> 105
 <211> 1856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (67)..(1233)

<400> 105
 attgctgggctg gctggcttcg gactgcgcgg gagctgccag gctgtccgcg ccgccgctgc 60
 ggggcc atg atc cgg aac ggg cgc ggg gct gca ggc ggc gca gag cag 108
 Met Ile Arg Asn Gly Arg Gly Ala Ala Gly Gly Ala Glu Gln
 1 5 10
 ccg ggc ccg ggg ggc agg cgc gcc gtg agg gtg tgg tgc gat ggc tgc 156
 Pro Gly Pro Gly Gly Arg Arg Ala Val Arg Val Trp Cys Asp Gly Cys
 15 20 25 30
 tat gac atg gtg cat tac ggc cac tcc aac cag ctg cgc cag gca cgg 204
 Tyr Asp Met Val His Tyr Gly His Ser Asn Gln Leu Arg Gln Ala Arg
 35 40 45

gcc atg ggt gac tac ctc atc gta ggc gtg cac acc gat gag gag atc	252
Ala Met Gly Asp Tyr Leu Ile Val Gly Val His Thr Asp Glu Glu Ile	
50 55 60	
gcc aag cac aag ggg ccc ccg gtg ttc act cag gag gag aga tac aag	300
Ala Lys His Lys Gly Pro Pro Val Phe Thr Gln Glu Glu Arg Tyr Lys	
65 70 75	
atg gtg cag gcc atc aaa tgg gtg gac gag gtg gtg cca gcg gct ccc	348
Met Val Gln Ala Ile Lys Trp Val Asp Glu Val Val Pro Ala Ala Pro	
80 85 90	
tac gtc act aca cta gag acc ctg gac aaa tac aac tgt gac ttc tgt	396
Tyr Val Thr Thr Leu Glu Thr Leu Asp Lys Tyr Asn Cys Asp Phe Cys	
95 100 105 110	
gtt cac ggc aat gac atc acc ctg act gta gat ggc cgg gac acc tat	444
Val His Gly Asn Asp Ile Thr Leu Thr Val Asp Gly Arg Asp Thr Tyr	
115 120 125	
gag gaa gta aag cag gct ggg agg tac aga gaa tgc aag cgc acg caa	492
Glu Glu Val Lys Gln Ala Gly Arg Tyr Arg Glu Cys Lys Arg Thr Gln	
130 135 140	
ggg gtg tcc acc aca gac ctc gtg ggc cgc atg ctg ctg gta acc aaa	540
Gly Val Ser Thr Thr Asp Leu Val Gly Arg Met Leu Leu Val Thr Lys	
145 150 155	
gcc cat cac agc agc cag gag atg tcc tct gag tac cgg gag tat gca	588
Ala His His Ser Ser Gln Glu Met Ser Ser Glu Tyr Arg Glu Tyr Ala	
160 165 170	
gac agt ttt ggc aag tgc cct ggt ggg cgg aac ccc tgg acc ggg gta	636
Asp Ser Phe Gly Lys Cys Pro Gly Gly Arg Asn Pro Trp Thr Gly Val	
175 180 185 190	
tcc cag ttc ctg cag aca tct cag aag atc atc cag ttt gct tct ggg	684
Ser Gln Phe Leu Gln Thr Ser Gln Lys Ile Ile Gln Phe Ala Ser Gly	
195 200 205	
aag gag ccc cag cca ggg gag aca gtc atc tat gtg gct ggt gcc ttc	732
Lys Glu Pro Gln Pro Gly Glu Thr Val Ile Tyr Val Ala Gly Ala Phe	
210 215 220	
gac ctg ttc cac atc ggg cat gtg gac ttc ctg gag aag gtg cac agg	780
Asp Leu Phe His Ile Gly His Val Asp Phe Leu Glu Lys Val His Arg	
225 230 235	
ctg gca gag agg ccc tac atc atc gcg ggc tta cac ttt gac cag gag	828
Leu Ala Glu Arg Pro Tyr Ile Ile Ala Gly Leu His Phe Asp Gln Glu	
240 245 250	
gtc aat cac tac aag ggg aag aac tac ccc atc atg aat ctg cat gaa	876
Val Asn His Tyr Lys Gly Lys Asn Tyr Pro Ile Met Asn Leu His Glu	
255 260 265 270	

cg	act	ctg	agc	gtg	ctg	gcc	tgc	cg	tac	gtg	tca	gaa	gtg	gtg	att	924
Arg	Thr	Leu	Ser	Val	Leu	Ala	Cys	Arg	Tyr	Val	Ser	Glu	Val	Val	Ile	
				275					280					285		
gga	gcc	ccg	tac	gcg	gtc	aca	gca	gag	ctc	cta	agt	cac	ttc	aag	gtg	972
Gly	Ala	Pro	Tyr	Ala	Val	Thr	Ala	Glu	Leu	Leu	Ser	His	Phe	Lys	Val	
				290				295					300			
gac	ctg	gtg	tgt	cac	ggc	aag	aca	gaa	att	atc	cct	gac	agg	gat	ggc	1020
Asp	Leu	Val	Cys	His	Gly	Lys	Thr	Glu	Ile	Ile	Pro	Asp	Arg	Asp	Gly	
				305			310					315				
tcc	gac	cca	tac	cag	gag	ccc	aag	aga	agg	ggc	atc	ttc	cgt	cag	att	1068
Ser	Asp	Pro	Tyr	Gln	Glu	Pro	Lys	Arg	Arg	Gly	Ile	Phe	Arg	Gln	Ile	
				320			325				330					
gac	agt	ggc	agc	aac	ctc	acc	aca	gac	ctc	atc	gtc	cag	cgg	atc	atc	1116
Asp	Ser	Gly	Ser	Asn	Leu	Thr	Thr	Asp	Leu	Ile	Val	Gln	Arg	Ile	Ile	
					340					345					350	
acc	aac	agg	ttg	gag	tat	gag	gcg	cga	aac	cag	aag	aag	gaa	gcc	aag	1164
Thr	Asn	Arg	Leu	Glu	Tyr	Glu	Ala	Arg	Asn	Gln	Lys	Lys	Glu	Ala	Lys	
				355					360					365		
gag	ctg	gcc	ttc	ctg	gag	gct	gcc	agg	cag	cag	gcg	gca	cag	ccc	ctg	1212
Glu	Leu	Ala	Phe	Leu	Glu	Ala	Ala	Arg	Gln	Gln	Ala	Ala	Gln	Pro	Leu	
				370				375					380			
ggg	gag	cgc	gat	ggg	gac	ttc	taacctggca	gaggccctgg	ccggccctcc							1263
Gly	Glu	Arg	Asp	Gly	Asp	Phe										
				385												
ccctgctctg	cttctgcgcc	ttctgcgttt	ggacatagga	ctctgcaggg	ccggccctctc											1323
taactggcct	ggctctggaa	gggctggtga	ggactctgcc	tccttgccctg	cctacaaggt											1383
gcttggtttg	cagcaggctc	tccgctcttt	ccagcaaagc	tgctcagaga	gggtgtccag											1443
cacagtggag	aggccggaag	tgagacgggc	agacggcacc	tgacgctga	aacgcaccgc											1503
tcctgcgtgc	gccccacct	ggtccccgga	tgccccacc	acctggacag	aggccacact											1563
gactgcccac	ccagctgtgg	cgggaggtgc	agagcagggg	gctttagggg	gcagtgactg											1623
cggtcacccc	tttagttctc	tgggtgtaga	ccacaccacc	tcccactggg	caccccccaa											1683
cacggtgtcc	tgccaccag	cgctggctc	caggaaaaca	cgcttgccctt	ccttcccggc											1743
agcttcgcca	ctctccttat	ggactctgtt	ctgtttgtac	atggctgacg	gaaatctctt											1803
tggtacaacc	gaataaagcc	tggtggcagt	gctgcgcggg	gctcccagcc	aat											1856
<210>	106															
<211>	389															
<212>	PRT															
<213>	Homo sapiens															

<400> 106

Met	Ile	Arg	Asn	Gly	Arg	Gly	Ala	Ala	Gly	Gly	Ala	Glu	Gln	Pro	Gly	1	5	10	15
Pro	Gly	Gly	Arg	Arg	Ala	Val	Arg	Val	Trp	Cys	Asp	Gly	Cys	Tyr	Asp	20	25	30	
Met	Val	His	Tyr	Gly	His	Ser	Asn	Gln	Leu	Arg	Gln	Ala	Arg	Ala	Met	35	40	45	
Gly	Asp	Tyr	Leu	Ile	Val	Gly	Val	His	Thr	Asp	Glu	Glu	Ile	Ala	Lys	50	55	60	
His	Lys	Gly	Pro	Pro	Val	Phe	Thr	Gln	Glu	Glu	Arg	Tyr	Lys	Met	Val	65	70	75	80
Gln	Ala	Ile	Lys	Trp	Val	Asp	Glu	Val	Val	Pro	Ala	Ala	Pro	Tyr	Val	85	90	95	
Thr	Thr	Leu	Glu	Thr	Leu	Asp	Lys	Tyr	Asn	Cys	Asp	Phe	Cys	Val	His	100	105	110	
Gly	Asn	Asp	Ile	Thr	Leu	Thr	Val	Asp	Gly	Arg	Asp	Thr	Tyr	Glu	Glu	115	120	125	
Val	Lys	Gln	Ala	Gly	Arg	Tyr	Arg	Glu	Cys	Lys	Arg	Thr	Gln	Gly	Val	130	135	140	
Ser	Thr	Thr	Asp	Leu	Val	Gly	Arg	Met	Leu	Leu	Val	Thr	Lys	Ala	His	145	150	155	160
His	Ser	Ser	Gln	Glu	Met	Ser	Ser	Glu	Tyr	Arg	Glu	Tyr	Ala	Asp	Ser	165	170	175	
Phe	Gly	Lys	Cys	Pro	Gly	Gly	Arg	Asn	Pro	Trp	Thr	Gly	Val	Ser	Gln	180	185	190	
Phe	Leu	Gln	Thr	Ser	Gln	Lys	Ile	Ile	Gln	Phe	Ala	Ser	Gly	Lys	Glu	195	200	205	
Pro	Gln	Pro	Gly	Glu	Thr	Val	Ile	Tyr	Val	Ala	Gly	Ala	Phe	Asp	Leu	210	215	220	
Phe	His	Ile	Gly	His	Val	Asp	Phe	Leu	Glu	Lys	Val	His	Arg	Leu	Ala	225	230	235	240
Glu	Arg	Pro	Tyr	Ile	Ile	Ala	Gly	Leu	His	Phe	Asp	Gln	Glu	Val	Asn	245	250	255	
His	Tyr	Lys	Gly	Lys	Asn	Tyr	Pro	Ile	Met	Asn	Leu	His	Glu	Arg	Thr	260	265	270	
Leu	Ser	Val	Leu	Ala	Cys	Arg	Tyr	Val	Ser	Glu	Val	Val	Ile	Gly	Ala	275	280	285	
Pro	Tyr	Ala	Val	Thr	Ala	Glu	Leu	Leu	Ser	His	Phe	Lys	Val	Asp	Leu	290	295	300	

Val Cys His Gly Lys Thr Glu Ile Ile Pro Asp Arg Asp Gly Ser Asp
 305 310 315 320

Pro Tyr Gln Glu Pro Lys Arg Arg Gly Ile Phe Arg Gln Ile Asp Ser
 325 330 335

Gly Ser Asn Leu Thr Thr Asp Leu Ile Val Gln Arg Ile Ile Thr Asn
 340 345 350

Arg Leu Glu Tyr Glu Ala Arg Asn Gln Lys Lys Glu Ala Lys Glu Leu
 355 360 365

Ala Phe Leu Glu Ala Ala Arg Gln Gln Ala Ala Gln Pro Leu Gly Glu
 370 375 380

Arg Asp Gly Asp Phe
 385

<210> 107
 <211> 1908
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (24)..(1718)

<400> 107
 gcagactcag ttcttgagaga aag atg gcg aca gcc gag aag cag aaa cac gac 53
 Met Ala Thr Ala Glu Lys Gln Lys His Asp
 1 5 10

ggg cgg gtg aag atc ggc cac tac att ctg ggt gac acg ctg ggg gtc 101
 Gly Arg Val Lys Ile Gly His Tyr Ile Leu Gly Asp Thr Leu Gly Val
 15 20 25

ggc acc ttc ggc aaa gtg aag gtt ggc aaa cat gaa ttg act ggg cat 149
 Gly Thr Phe Gly Lys Val Lys Val Gly Lys His Glu Leu Thr Gly His
 30 35 40

aaa gta gct gtg aag ata ctc aat cga cag aag att cgg agc ctt gat 197
 Lys Val Ala Val Lys Ile Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp
 45 50 55

gtg gta gga aaa atc cgc aga gaa att cag aac ctc aag ctt ttc agg 245
 Val Val Gly Lys Ile Arg Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg
 60 65 70

cat cct cat ata att aaa ctg tac cag gtc atc agt aca cca tct gat 293
 His Pro His Ile Ile Lys Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp
 75 80 85 90

att ttc atg gtg atg gaa tat gtc tca gga gga gag cta ttt gat tat 341
 Ile Phe Met Val Met Glu Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr
 95 100 105

atc tgt aag aat gga agg aaa tct gat gta cct gga gta gta aaa aca	389
Ile Cys Lys Asn Gly Arg Lys Ser Asp Val Pro Gly Val Val Lys Thr	
110 115 120	
ggc tcc acg aag gag ctg gat gaa aaa gaa agt cgg cgt ctg ttc caa	437
Gly Ser Thr Lys Glu Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln	
125 130 135	
cag atc ctt tct ggt gtg gat tat tgt cac agg cat atg gtg gtc cat	485
Gln Ile Leu Ser Gly Val Asp Tyr Cys His Arg His Met Val Val His	
140 145 150	
aga gat ttg aaa cct gaa aat gtc ctg ctt gat gca cac atg aat gca	533
Arg Asp Leu Lys Pro Glu Asn Val Leu Leu Asp Ala His Met Asn Ala	
155 160 165 170	
aag ata gct gat ttt ggt ctt tca aac atg atg tca gat ggt gaa ttt	581
Lys Ile Ala Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe	
175 180 185	
tta aga aca agt tgt ggc tca ccc aac tat gct gca cca gaa gta att	629
Leu Arg Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile	
190 195 200	
tca gga aga ttg tat gca ggc cca gag gta gat ata tgg agc agt ggg	677
Ser Gly Arg Leu Tyr Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly	
205 210 215	
gtt att ctc tat gct tta tta tgt gga acc ctt cca ttt gat gat gac	725
Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp	
220 225 230	
cat gtg cca act ctt ttt aag aag ata tgt gat ggg atc ttc tat acc	773
His Val Pro Thr Leu Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr	
235 240 245 250	
cct caa tat tta aat cct tct gtg att agc ctt ttg aaa cat atg ctg	821
Pro Gln Tyr Leu Asn Pro Ser Val Ile Ser Leu Leu Lys His Met Leu	
255 260 265	
cag gtg gat ccc atg aag agg gcc tca atc aaa gat atc agg gaa cat	869
Gln Val Asp Pro Met Lys Arg Ala Ser Ile Lys Asp Ile Arg Glu His	
270 275 280	
gaa tgg ttt aaa cag gac ctt cca aaa tat ctc ttt cct gag gat cca	917
Glu Trp Phe Lys Gln Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro	
285 290 295	
tca tat agt tca acc atg att gat gat gaa gcc tta aaa gaa gta tgt	965
Ser Tyr Ser Ser Thr Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys	
300 305 310	
gaa aag ttt gag tgc tca gaa gag gaa gtt ctc agc tgt ctt tac aac	1013
Glu Lys Phe Glu Cys Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn	
315 320 325 330	
aga aat cac cag gat cct ttg gca gtt gcc tac cat ctc ata ata gat	1061

Arg	Asn	His	Gln	Asp	Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	
				335					340						345	
aac	agg	aga	ata	atg	aat	gaa	gcc	aaa	gat	ttc	tat	ttg	gcg	aca	agc	1109
Asn	Arg	Arg	Ile	Met	Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	
			350					355					360			
cca	cct	gat	tct	ttt	ctt	gat	gat	cat	cac	ctg	act	cgg	ccc	cat	cct	1157
Pro	Pro	Asp	Ser	Phe	Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	
			365				370					375				
gaa	aga	gta	cca	ttc	ttg	gtt	gct	gaa	aca	cca	agg	gca	cgc	cat	acc	1205
Glu	Arg	Val	Pro	Phe	Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	
	380					385					390					
ctt	gat	gaa	tta	aat	cca	cag	aaa	tcc	aaa	cac	caa	ggg	gta	agg	aaa	1253
Leu	Asp	Glu	Leu	Asn	Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	
395				400					405						410	
gca	aaa	tgg	cat	tta	gga	att	aga	agt	caa	agt	cga	cca	aat	gat	att	1301
Ala	Lys	Trp	His	Leu	Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	
			415					420					425			
atg	gca	gaa	gta	tgt	aga	gca	atc	aaa	caa	ttg	gat	tat	gaa	tgg	aag	1349
Met	Ala	Glu	Val	Cys	Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	
			430				435					440				
gtt	gta	aac	cca	tat	tat	ttg	cgt	gta	cga	agg	aag	aat	cct	gtg	aca	1397
Val	Val	Asn	Pro	Tyr	Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	
		445				450					455					
agc	act	tac	tcc	aaa	atg	agt	cta	cag	tta	tac	caa	gtg	gat	agt	aga	1445
Ser	Thr	Tyr	Ser	Lys	Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	
	460					465				470						
act	tat	cta	ctg	gat	ttc	cgt	agt	att	gat	gat	gaa	att	aca	gaa	gcc	1493
Thr	Tyr	Leu	Leu	Asp	Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	
475				480				485						490		
aaa	tca	ggg	act	gct	act	cca	cag	aga	tcg	gga	tca	gtt	agc	aac	tat	1541
Lys	Ser	Gly	Thr	Ala	Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	
			495					500					505			
cga	tct	tgc	caa	agg	agt	gat	tca	gat	gct	gag	gct	caa	gga	aaa	tcc	1589
Arg	Ser	Cys	Gln	Arg	Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	
			510				515					520				
tca	gaa	gtt	tct	ctt	acc	tca	tct	gtg	acc	tca	ctt	gac	tct	tct	cct	1637
Ser	Glu	Val	Ser	Leu	Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	
		525				530					535					
gtt	gac	cta	act	cca	aga	cct	gga	agt	cac	aca	ata	gaa	ttt	ttt	gag	1685
Val	Asp	Leu	Thr	Pro	Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	
	540					545				550						
atg	tgt	gca	aat	cta	att	aaa	att	ctt	gca	caa	taa	acagaaa	actttgctta			1738
Met	Cys	Ala	Asn	Leu	Ile	Lys	Ile	Leu	Ala	Gln						

225					230					235				240	
Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn	Pro
				245					250					255	
Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met	Lys
			260					265					270		
Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln	Asp
		275					280					285			
Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr	Met
	290					295					300				
Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys	Ser
305					310					315					320
Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp	Pro
				325					330					335	
Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met	Asn
			340					345					350		
Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe	Leu
		355					360					365			
Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe	Leu
	370					375					380				
Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn	Pro
385					390					395					400
Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu	Gly
				405					410					415	
Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys	Arg
			420					425					430		
Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr	Tyr
		435					440					445			
Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys	Met
	450					455					460				
Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp	Phe
465					470					475					480
Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala	Thr
				485					490					495	
Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg	Ser
			500					505					510		
Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu	Thr
		515					520					525			
Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro	Arg

530		535		540	
Pro Gly Ser His Thr	Ile Glu Phe Phe Glu Met Cys Ala Asn Leu Ile				
545	550	555		560	
Lys Ile Leu Ala Gln					
	565				
<210> 109					
<211> 1863					
<212> DNA					
<213> Homo sapiens					
<220>					
<221> CDS					
<222> (24) .. (1673)					
<400> 109					
cgagactcag	ttcctggaga	aag atg gcg	aca gcc gag	aag cag aaa	cac gac 53
		Met Ala Thr	Ala Glu Lys	Gln Lys His	Asp
		1	5		10
ggg cgg gtg aag atc	ggc cac tac att	ctg ggt gac	acg ctg ggg	gtc	101
Gly Arg Val Lys	Ile Gly His Tyr	Ile Leu Gly	Asp Thr Leu	Gly Val	
	15	20	25		
ggc acc ttc ggc aaa	gtg aag gtt ggc	aaa cat gaa	ttg act ggg	cat	149
Gly Thr Phe Gly	Lys Val Lys Val	Gly Lys His	Glu Leu Thr	Gly His	
	30	35	40		
aaa gta gct gtg aag	ata ctc aat cga	cag aag att	cgg agc ctt	gat	197
Lys Val Ala Val	Lys Ile Leu Asn	Arg Gln Lys	Ile Arg Ser	Leu Asp	
	45	50	55		
gtg gta gga aaa atc	cgc aga gaa att	cag aac ctc	aag ctt ttc	agg	245
Val Val Gly Lys	Ile Arg Arg Glu	Ile Gln Asn	Leu Lys Leu	Phe Arg	
	60	65	70		
cat cct cat ata att	aaa ctg tac cag	gtc atc agt	aca cca tct	gat	293
His Pro His Ile	Ile Lys Leu Tyr	Gln Val Ile	Ser Thr Pro	Ser Asp	
	75	80	85	90	
att ttc atg gtg atg	gaa tat gtc tca	gga gga gag	cta ttt gat	tat	341
Ile Phe Met Val	Met Glu Tyr Val	Ser Gly Gly	Glu Leu Phe	Asp Tyr	
	95	100	105		
atc tgt aag aat gga	agg ctg gat gaa	aaa gaa agt	cgg cgt ctg	ttc	389
Ile Cys Lys Asn	Gly Arg Leu Asp	Glu Lys Glu	Ser Arg Arg	Leu Phe	
	110	115	120		
caa cag atc ctt tct	ggt gtg gat tat	tgt cac agg	cat atg gtg	gtc	437
Gln Gln Ile Leu	Ser Gly Val Asp	Tyr Cys His	Arg His Met	Val Val	
	125	130	135		
cat aga gat ttg aaa	cct gaa aat gtc	ctg ctt gat	gca cac atg	aat	485
His Arg Asp Leu	Lys Pro Glu Asn	Val Leu Leu	Asp Ala His	Met Asn	
	140	145	150		

gca aag ata gct gat ttt ggt ctt tca aac atg atg tca gat ggt gaa	533
Ala Lys Ile Ala Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu	
155 160 165 170	
ttt tta aga aca agt tgt ggc tca ccc aac tat gct gca cca gaa gta	581
Phe Leu Arg Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val	
175 180 185	
att tca gga aga ttg tat gca ggc cca gag gta gat ata tgg agc agt	629
Ile Ser Gly Arg Leu Tyr Ala Gly Pro Glu Val Asp Ile Trp Ser Ser	
190 195 200	
ggg gtt att ctc tat gct tta tta tgt gga acc ctt cca ttt gat gat	677
Gly Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp	
205 210 215	
gac cat gtg cca act ctt ttt aag aag ata tgt gat ggg atc ttc tat	725
Asp His Val Pro Thr Leu Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr	
220 225 230	
acc cct caa tat tta aat cct tct gtg att agc ctt ttg aaa cat atg	773
Thr Pro Gln Tyr Leu Asn Pro Ser Val Ile Ser Leu Leu Lys His Met	
235 240 245 250	
ctg cag gtg gat ccc atg aag agg gcc tca atc aaa gat atc agg gaa	821
Leu Gln Val Asp Pro Met Lys Arg Ala Ser Ile Lys Asp Ile Arg Glu	
255 260 265	
cat gaa tgg ttt aaa cag gac ctt cca aaa tat ctc ttt cct gag gat	869
His Glu Trp Phe Lys Gln Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp	
270 275 280	
cca tca tat agt tca acc atg att gat gat gaa gcc tta aaa gaa gta	917
Pro Ser Tyr Ser Ser Thr Met Ile Asp Asp Glu Ala Leu Lys Glu Val	
285 290 295	
tgt gaa aag ttt gag tgc tca gaa gag gaa gtt ctc agc tgt ctt tac	965
Cys Glu Lys Phe Glu Cys Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr	
300 305 310	
aac aga aat cac cag gat cct ttg gca gtt gcc tac cat ctc ata ata	1013
Asn Arg Asn His Gln Asp Pro Leu Ala Val Ala Tyr His Leu Ile Ile	
315 320 325 330	
gat aac agg aga ata atg aat gaa gcc aaa gat ttc tat ttg gcg aca	1061
Asp Asn Arg Arg Ile Met Asn Glu Ala Lys Asp Phe Tyr Leu Ala Thr	
335 340 345	
agc cca cct gat tct ttt ctt gat gat cat cac ctg act cgg ccc cat	1109
Ser Pro Pro Asp Ser Phe Leu Asp Asp His His Leu Thr Arg Pro His	
350 355 360	
cct gaa aga gta cca ttc ttg gtt gct gaa aca cca agg gca cgc cat	1157
Pro Glu Arg Val Pro Phe Leu Val Ala Glu Thr Pro Arg Ala Arg His	
365 370 375	

acc ctt gat gaa tta aat cca cag aaa tcc aaa cac caa ggt gta agg	1205
Thr Leu Asp Glu Leu Asn Pro Gln Lys Ser Lys His Gln Gly Val Arg	
380 385 390	
aaa gca aaa tgg cat tta gga att aga agt caa agt cga cca aat gat	1253
Lys Ala Lys Trp His Leu Gly Ile Arg Ser Gln Ser Arg Pro Asn Asp	
395 400 405 410	
att atg gca gaa gta tgt aga gca atc aaa caa ttg gat tat gaa tgg	1301
Ile Met Ala Glu Val Cys Arg Ala Ile Lys Gln Leu Asp Tyr Glu Trp	
415 420 425	
aag gtt gta aac cca tat tat ttg cgt gta cga agg aag aat cct gtg	1349
Lys Val Val Asn Pro Tyr Tyr Leu Arg Val Arg Arg Lys Asn Pro Val	
430 435 440	
aca agc act tac tcc aaa atg agt cta cag tta tac caa gtg gat agt	1397
Thr Ser Thr Tyr Ser Lys Met Ser Leu Gln Leu Tyr Gln Val Asp Ser	
445 450 455	
aga act tat cta ctg gat ttc cgt agt att gat gat gaa att aca gaa	1445
Arg Thr Tyr Leu Leu Asp Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu	
460 465 470	
gcc aaa tca ggg act gct act cca cag aga tcg gga tca gtt agc aac	1493
Ala Lys Ser Gly Thr Ala Thr Pro Gln Arg Ser Gly Ser Val Ser Asn	
475 480 485 490	
tat cga tct tgc caa agg agt gat tca gat gct gag gct caa gga aaa	1541
Tyr Arg Ser Cys Gln Arg Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys	
495 500 505	
tcc tca gaa gtt tct ctt acc tca tct gtg acc tca ctt gac tct tct	1589
Ser Ser Glu Val Ser Leu Thr Ser Ser Val Thr Ser Leu Asp Ser Ser	
510 515 520	
cct gtt gac cta act cca aga cct gga agt cac aca ata gaa ttt ttt	1637
Pro Val Asp Leu Thr Pro Arg Pro Gly Ser His Thr Ile Glu Phe Phe	
525 530 535	
gag atg tgt gca aat cta att aaa att ctt gca caa taaacagaaa	1683
Glu Met Cys Ala Asn Leu Ile Lys Ile Leu Ala Gln	
540 545 550	
actttgctta tttcttttgc agcaataagc atgcataata agtcacagcc aaatgcttcc	1743
atttgtaatc aagttataca taattataac cgaggggctgg cgtttttgaa tcgaatttcg	1803
acaggggattg gaacatgatt tatagttaaaa agcctaatat cgagaaatga attaagatca	1863
<210> 110	
<211> 550	
<212> PRT	
<213> Homo sapiens	
<400> 110	
Met Ala Thr Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly	

1	5	10	15
His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val	20	25	30
Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile	35	40	45
Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg	50	55	60
Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys	65	70	75
Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu	85	90	95
Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg	100	105	110
Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly	115	120	125
Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro	130	135	140
Glu Asn Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe	145	150	155
Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys	165	170	175
Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr	180	185	190
Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly Val Ile Leu Tyr Ala	195	200	205
Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp His Val Pro Thr Leu	210	215	220
Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr Pro Gln Tyr Leu Asn	225	230	235
Pro Ser Val Ile Ser Leu Leu Lys His Met Leu Gln Val Asp Pro Met	245	250	255
Lys Arg Ala Ser Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln	260	265	270
Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Ser Ser Thr	275	280	285
Met Ile Asp Asp Glu Ala Leu Lys Glu Val Cys Glu Lys Phe Glu Cys	290	295	300
Ser Glu Glu Glu Val Leu Ser Cys Leu Tyr Asn Arg Asn His Gln Asp			

305		310		315		320									
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met
				325					330					335	
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe
			340					345					350		
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe
		355					360					365			
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn
	370					375					380				
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu
385					390					395					400
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys
				405					410					415	
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr
			420					425					430		
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys
		435					440					445			
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp
	450					455					460				
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala
465				470					475					480	
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg
				485					490					495	
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu
			500					505					510		
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro
		515					520					525			
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu
	530					535					540				
Ile	Lys	Ile	Leu	Ala	Gln										
545					550										

<210> 111
 <211> 1863
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (24) .. (1673)

<400> 111

gcagactcag ttcctggaga aag atg gcg aca gcc gag aag cag aaa cac gac 53
Met Ala Thr Ala Glu Lys Gln Lys His Asp
1 5 10

ggg cgg gtg aag atc ggc cac tac att ctg ggt gac acg ctg ggg gtc 101
Gly Arg Val Lys Ile Gly His Tyr Ile Leu Gly Asp Thr Leu Gly Val
15 20 25

ggc acc ttc ggc aaa gtg aag gtt ggc aaa cat gaa ttg act ggg cat 149
Gly Thr Phe Gly Lys Val Lys Val Gly Lys His Glu Leu Thr Gly His
30 35 40

aaa gta gct gtg aag ata ctc aat cga cag aag att cgg agc ctt gat 197
Lys Val Ala Val Lys Ile Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp
45 50 55

gtg gta gga aaa atc cgc aga gaa att cag aac ctc aag ctt ttc agg 245
Val Val Gly Lys Ile Arg Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg
60 65 70

cat cct cat ata att aaa ctg tac cag gtc atc agt aca cca tct gat 293
His Pro His Ile Ile Lys Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp
75 80 85 90

att ttc atg gtg atg gaa tat gtc tca gga gga gag cta ttt gat tat 341
Ile Phe Met Val Met Glu Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr
95 100 105

atc tgt aag aat gga agg ctg gat gaa aaa gaa agt cgg cgt ctg ttc 389
Ile Cys Lys Asn Gly Arg Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe
110 115 120

caa cag atc ctt tct ggt gtg gat tat tgt cac agg cat atg gtg gtc 437
Gln Gln Ile Leu Ser Gly Val Asp Tyr Cys His Arg His Met Val Val
125 130 135

cat aga gat ttg aaa cct gaa aat gtc ctg ctt gat gca cac atg aat 485
His Arg Asp Leu Lys Pro Glu Asn Val Leu Leu Asp Ala His Met Asn
140 145 150

gca aag ata gct gat ttt ggt ctt tca aac atg atg tca gat ggt gaa 533
Ala Lys Ile Ala Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu
155 160 165 170

ttt tta aga aca agt tgt ggc tca ccc aac tat gct gca cca gaa gta 581
Phe Leu Arg Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val
175 180 185

att tca gga aga ttg tat gca ggc cca gag gta gat ata tgg agc agt 629
Ile Ser Gly Arg Leu Tyr Ala Gly Pro Glu Val Asp Ile Trp Ser Ser
190 195 200

ggg gtt att ctc tat gct tta tta tgt gga acc ctt cca ttt gat gat 677
Gly Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp
205 210 215

gac cat gtg cca act ctt ttt aag aag ata tgt gat ggg atc ttc tat 725

Asp	His	Val	Pro	Thr	Leu	Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr		
220						225					230						
acc	cct	caa	tat	tta	aat	cct	tct	gtg	att	agc	ctt	ttg	aaa	cat	atg	773	
Thr	Pro	Gln	Tyr	Leu	Asn	Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met		
235					240					245					250		
ctg	cag	gtg	gat	ccc	atg	aag	agg	gcc	tca	atc	aaa	gat	atc	agg	gaa	821	
Leu	Gln	Val	Asp	Pro	Met	Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu		
				255				260						265			
cat	gaa	tgg	ttt	aaa	cag	gac	ctt	cca	aaa	tat	ctc	ttt	cct	gag	gat	869	
His	Glu	Trp	Phe	Lys	Gln	Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp		
			270					275					280				
cca	tca	tat	agt	tca	acc	atg	att	gat	gat	gaa	gcc	tta	aaa	gaa	gta	917	
Pro	Ser	Tyr	Ser	Ser	Thr	Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val		
		285					290					295					
tgt	gaa	aag	ttt	gag	tgc	tca	gaa	gag	gaa	gtt	ctc	agc	tgt	ctt	tac	965	
Cys	Glu	Lys	Phe	Glu	Cys	Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr		
	300					305					310						
aac	aga	aat	cac	cag	gat	cct	ttg	gca	gtt	gcc	tac	cat	ctc	ata	ata	1013	
Asn	Arg	Asn	His	Gln	Asp	Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile		
315					320					325					330		
gat	aac	agg	aga	ata	atg	aat	gaa	gcc	aaa	gat	ttc	tat	ttg	gcg	aca	1061	
Asp	Asn	Arg	Arg	Ile	Met	Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr		
				335					340					345			
agc	cca	cct	gat	tct	ttt	ctt	gat	gat	cat	cac	ctg	act	cgg	ccc	cat	1109	
Ser	Pro	Pro	Asp	Ser	Phe	Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His		
			350					355					360				
cct	gaa	aga	gta	cca	ttc	ttg	gtt	gct	gaa	aca	cca	agg	gca	cgc	cat	1157	
Pro	Glu	Arg	Val	Pro	Phe	Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His		
		365					370					375					
acc	ctt	gat	gaa	tta	aat	cca	cag	aaa	tcc	aaa	cac	caa	ggg	gta	agg	1205	
Thr	Leu	Asp	Glu	Leu	Asn	Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg		
	380					385					390						
aaa	gca	aaa	tgg	cat	tta	gga	att	aga	agt	caa	agt	cga	cca	aat	gat	1253	
Lys	Ala	Lys	Trp	His	Leu	Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp		
	395				400					405					410		
att	atg	gca	gaa	gta	tgt	aga	gca	atc	aaa	caa	ttg	gat	tat	gaa	tgg	1301	
Ile	Met	Ala	Glu	Val	Cys	Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp		
				415					420					425			
aag	gtt	gta	aac	cca	tat	tat	ttg	cgt	gta	cga	agg	aag	aat	cct	gtg	1349	
Lys	Val	Val	Asn	Pro	Tyr	Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val		
			430					435					440				
aca	agc	act	tac	tcc	aaa	atg	agt	cta	cag	tta	tac	caa	gtg	gat	agt	1397	
Thr	Ser	Thr	Tyr	Ser	Lys	Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser		

445	450	455	
aga act tat cta ctg gat ttc cgt agt att gat gat gaa att aca gaa			1445
Arg Thr Tyr Leu Leu Asp Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu			
460	465	470	
gcc aaa tca ggg act gct act cca cag aga tcg gga tca gtt agc aac			1493
Ala Lys Ser Gly Thr Ala Thr Pro Gln Arg Ser Gly Ser Val Ser Asn			
475	480	485	490
tat cga tct tgc caa agg agt gat tca gat gct gag gct caa gga aaa			1541
Tyr Arg Ser Cys Gln Arg Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys			
	495	500	505
tcc tca gaa gtt tct ctt acc tca tct gtg acc tca ctt gac tct tct			1589
Ser Ser Glu Val Ser Leu Thr Ser Ser Val Thr Ser Leu Asp Ser Ser			
	510	515	520
cct gtt gac cta act cca aga cct gga agt cac aca ata gaa ttt ttt			1637
Pro Val Asp Leu Thr Pro Arg Pro Gly Ser His Thr Ile Glu Phe Phe			
	525	530	535
gag atg tgt gca aat cta att aaa att ctt gca caa taaacagaaa			1683
Glu Met Cys Ala Asn Leu Ile Lys Ile Leu Ala Gln			
540	545	550	
actttgctta tttcttttgc agcaataagc atgcataata agtcacagcc aaatgcttcc 1743			
atttgtaatc aagttataca taattataac cgagggctgg cgttttggaa tcgaatttcg 1803			
acagggattg gaacatgatt tatagttaaa agcctaatat cgagaaatga attaagatca 1863			
<210> 112			
<211> 550			
<212> PRT			
<213> Homo sapiens			
<400> 112			
Met Ala Thr Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly			
1	5	10	15
His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val			
	20	25	30
Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile			
	35	40	45
Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg			
	50	55	60
Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys			
	65	70	75
Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu			
	85	90	95
Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg			

100					105					110					
Leu	Asp	Glu	Lys	Glu	Ser	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Gly
		115					120					125			
Val	Asp	Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro
		130					135					140			
Glu	Asn	Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe
145							150					155			160
Gly	Leu	Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys
				165					170					175	
Gly	Ser	Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr
			180					185					190		
Ala	Gly	Pro	Glu	Val	Asp	Ile	Trp	Ser	Ser	Gly	Val	Ile	Leu	Tyr	Ala
		195					200					205			
Leu	Leu	Cys	Gly	Thr	Leu	Pro	Phe	Asp	Asp	Asp	His	Val	Pro	Thr	Leu
		210					215					220			
Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn
225							230					235			240
Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met
				245					250					255	
Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln
			260					265					270		
Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr
		275					280					285			
Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys
		290					295					300			
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp
305							310					315			320
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met
				325					330					335	
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe
			340					345					350		
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe
		355					360					365			
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn
		370					375					380			
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu
385							390					395			400
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys

405					410					415						
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr	
420					425					430						
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys	
435					440					445						
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp	
450					455					460						
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala	
465					470					475					480	
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg	
485					490					495						
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu	
500					505					510						
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro	
515					520					525						
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu	
530					535					540						
Ile	Lys	Ile	Leu	Ala	Gln											
545					550											

<210> 113
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 113
 aaagttcaat gccaggagaa ag 22

<210> 114
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 114
 taagggagcc atcctcacca cca 23

<210> 115
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 115
aaactcttgg ctgagaaatt cc 22

<210> 116
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: Primer/Probe

<400> 116
tccatacaga tcaccaactg tg 22

<210> 117
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: Primer/Probe

<400> 117
tcgtccgaac tcttcccctt gcttc 25

<210> 118
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: Primer/Probe

<400> 118
agacattatg gaacgtggag a 21

<210> 119
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: Primer/Probe

<400> 119
cttcagcttc tctttccctt gt 22

<210> 120
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artifical Sequence: Primer/Probe

<400> 120
 tcttggacag gagcaccctc atttcc 26

<210> 121
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 121
 acaccactgc acctaaaacc tt 22

<210> 122
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 122
 tagaatctgc cgtcttttga ag 22

<210> 123
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 123
 tcaccctaatt attgtgcgac ttcattg 26

<210> 124
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 124
 ccaagtagtg aaagccctct tc 22

<210> 125
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 125
 aaggcctcca ccgacat 17

<210> 126
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 126
 tatcgtcttc actgccacct tgggtg 25

 <210> 127
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 127
 gaccactaca agaccaccta caac 24

 <210> 128
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 128
 gcggaagaag aagccatata at 22

 <210> 129
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 129
 ttacaccaag aggaatgctc ttcgcg 26

 <210> 130
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 130
 gagacttgta atcgtccatc ca 22

 <210> 131

<211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 131
 cctgtgttgt ttgccagtt 20

 <210> 132
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 132
 taaggcgaga caatacacat tccaac 26

 <210> 133
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 133
 cttgccagct taggaccatt 20

 <210> 134
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 134
 agctcttctt tgtcaaatac ttcca 25

 <210> 135
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 135
 taccctggct catcagcttt gcacta 26

 <210> 136
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 136
 agaaacctca tatcaagcct cttc 24

<210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 137
 catcttccgt cagattgaca gt 22

<210> 138
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 138
 tagcaacctc accacagacc tcatcg 26

<210> 139
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 139
 atactccaac ctgttggtga tg 22

<210> 140
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: Primer/Probe

<400> 140
 aacagaaatc accaggatcc tt 22

<210> 141
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 141
 ttggcagttg cctaccatct cataat 26

 <210> 142
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 142
 tgtcgccaaa tagaaatctt tg 22

 <210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 143
 accatctgat attttcatgg tgat 24

 <210> 144
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 144
 ttcaaatagc tctcctcctg agacatattc 30

 <210> 145
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

 <400> 145
 gtacatcaga tttccttcca ttcttac 27

 <210> 146
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artifical Sequence: Primer/Probe

<400> 146

tcttaccag aaatctagag gatctctct

30